

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 10:04:46 : Search time 2818 Seconds  
(without alignments)  
18881.523 Million cell updates/sec

Title: US-10-016-248-1  
Perfect score: 10136  
Sequence: 1 atgcgcggcgcccccctccccc.....ctcgaagcgcgccacgcgcac 10136

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04\*

1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10136	100.0	10136	6	ABSG64375 Human club
2	10136	100.0	10136	12	ADH71137 Human gen
3	10134.4	100.0	10136	12	ADH71165 Human gen
4	10132.8	100.0	10136	12	ADH71167 Human gen
5	9710.4	95.8	9951	12	ADH71141 Human gen
6	9508	93.8	10655	12	ADH71135 Human gen
7	9120	90.0	10466	12	ADH71143 Human gen
8	8760.4	86.4	12900	12	ADH71145 Human gen
9	7616.4	75.1	8010	12	ADH71139 Human gen
10	7614.8	75.1	8010	12	ABSG64376 Human gen
11	4260.4	42.0	6004	6	AA149944 Human mol
12	4183.2	41.3	12525	6	AAAD3319 Human C3b/C
13	4174.2	41.1	10989	12	ADH72215 Human gen
14	4067.4	40.1	10433	6	AAAD33320 Human C3b
15	4067.4	40.1	10673	6	AAAD33318 Human C3b
16	3597.8	35.5	3896	4	AAAF87127 NOV16 cod
17	3597.8	35.5	3896	12	ADH71163 Human gen
18	3561.8	35.1	3905	4	AAAF87126 NOV15 cod
19	3549.8	35.0	3904	12	ADH71161 Human gen
20	2716	26.8	8034	6	AAAS18806 DNA encod
21	2715.4	26.8	7333	6	AAAS18805 DNA encod

#### ALIGNMENTS

22	2671	26.4	6409	6	AAAS18803	AAAS18803 DNA encod
23	2595	25.6	2607	12	ADH71153	ADH71153 Human gen
24	2503.6	24.7	5598	6	AAAS18801	AAAS18801 DNA encod
25	2482.6	24.5	2997	10	ADC30517	ADC30517 Human nov
26	2450.8	24.2	5667	6	AAAS18804	AAAS18804 DNA encod
27	2450.2	24.2	6145	6	AAAS18802	AAAS18802 DNA encod
28	2331	22.8	2328	12	ADH71149	ADH71149 Human gen
29	2303	22.7	2329	12	ADH71147	ADH71147 Human gen
30	2122.4	20.9	2487	4	AAAS00146	AAAS00146 Human cdn
31	1919.8	18.9	2139	12	ADH71151	ADH71151 Human gen
32	1776.8	17.5	1792	12	ADH71157	ADH71157 Human gen
33	1569	15.5	3810	11	ADM02129	ADM02129 Human cdn
34	1442.8	14.2	4506	6	ABSS58378	ABSS58378 Protein m
35	1371.6	13.5	2387	6	ABNS9361	ABNS9361 Human sec
36	1031.2	10.2	1615	6	ABA00063	ABA00063 CADHP-10
37	978.4	9.7	2026	10	ADC30413	ADC30413 Human nov
38	954.2	9.4	3019	12	ADH72219	ADH72219 Human gen
39	852	8.4	1749	10	ADC30885	ADC30885 Human nov
40	796.2	7.9	3117	8	ABX34721	ABX34721 Human int
41	783.6	7.7	2609	6	AAAD37600	AAAD37600 Human int
42	733.8	7.2	1135	4	AAAF83001	AAAF83001 Human MBS
43	733.8	7.2	1135	12	ADH71159	ADH71159 Human gen
44	594.8	5.9	894	8	ACD05597	ACD05597 cDNA enco
45	585.4	5.8	3145	8	ABX72185	ABX72185 Human NOV

#### RESULT 1

ABSG64375 standard; DNA; 10136 BP.

ABSG64375;

15-NOV-2002 (first entry)

Human club and sushi domain containing gene #1.

KW Human; NOVX; neurodegenerative disease; Alzheimer's disease; anxiety;  
KW Parkinson's disease; Huntington's disease; neurological disorder;  
KW schizophrenia; manic depression; mental retardation; angina pectoris;  
KW cardiovascular disease; acute heart failure; myocardial infarction;  
KW muscular disease; muscular disorder; retinal disease; photoreception;  
KW deafness; keratinisation disorder; cancer; ovarian cancer; melanoma;  
KW immunological disorder; inflammatory disease; immune disease; diabetes;  
KW bacterial infection; fungal infection; protozoal infection; obesity;  
KW viral infection; reproductive system disorder; metabolic disturbance;  
KW anorexia; wasting disorder; chronic disease; infectious disease;  
KW dyslipidaemia; club; sushi; myelin; von Willebrand factor; kielin;  
KW semaphorin; serine/threonine protein kinase; TGF-beta binding;  
KW mas proto-oncogene; ribonuclease pancreatic precursor; aminotransferase;  
KW tollid-like 2; cysteine sulfonic acid decarboxylase; gene; ds;  
KW single nucleotide polymorphism; SNP.

Homo sapiens.

Key Location/Qualifiers

variation replace(3082,A)

variation /tag= a

variation /note= "Single nucleotide polymorphism (SNP)"

variation /tag= b

variation /note= "Single nucleotide polymorphism (SNP)"

variation /tag= c

variation /note= "Single nucleotide polymorphism (SNP)"

variation /tag= d

variation /note= "Single nucleotide polymorphism (SNP)"

MO200264791-A2.

PD 22-AUG-2002.  
 XX 10-DEC-2001; 2001WO-US048369.  
 XX 08-DEC-2000; 2000US-0254329P.  
 PR 14-DEC-2000; 2000US-0255648P.  
 PR 15-MAY-2001; 2001US-0291037P.  
 PR 08-JUN-2001; 2001US-0291713P.  
 PR 08-JUN-2001; 2001US-0309258P.  
 PR 29-AUG-2001; 2001US-0315639P.  
 PR 01-OCT-2001; 2001US-0326393P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Alsbrook JP, Anderson DW, Burgess CE, Boidog FL, Casman SJ,  
 PI Colman SP, Edinger SR, Ellerman K, Gerlach V, Gorman H, Grosse WM,  
 PI Guo X, Herrman JJ, Kekuda R, Lepley DW, Li L, Macdougall JR,  
 PI Miller I, Pena CE, Peyman JA, Rastelli L, Rieger DK, Shinkets RA,  
 PI Smithson G, Spylek KA, Stone DJ, Tchernev VT, Vernet CAM, Voss EZ,  
 PI Zernhusen BD, Zhong H, Zhong M;  
 XX  
 DR WPI; 2002-643486/69.  
 DR P-PSDB; ABG79168.  
 XX  
 PT New NOVX polypeptides and polynucleotides useful for treating or  
 PT preventing e.g. neurodegenerative diseases, neurological disorders,  
 PT cardiovascular diseases, muscular diseases and disorders, or  
 PT immunological diseases.  
 XX  
 PS Claim 9; Page 10-12; 29pp; English.  
 XX  
 CC The present invention relates to new NOVX polypeptides. The polypeptides,  
 CC polynucleotides and antibodies are useful in the manufacture of a  
 CC medicament for treating or preventing neurodegenerative diseases (e.g.  
 CC Alzheimer's disease, Parkinson's disease, or Huntington's disease),  
 CC neurological disorders (e.g. anxiety, schizophrenia, manic depression or  
 CC mental retardation), cardiovascular disease (e.g. acute heart failure,  
 CC angina pectoris or myocardial infarction), muscular diseases and  
 CC disorders, retinal diseases (including those involving photoreception,  
 CC deafness and keratinisation disorders), cancer (e.g. ovarian cancer or  
 CC melanoma), immunological disorders, inflammatory and immune diseases,  
 CC system disorders. The proteins of the invention may be used to screen  
 CC drugs or compounds that modulate the NOVX protein activity or expression,  
 CC as well as to treat disorders characterised by insufficient or excessive  
 CC production of NOVX protein or protein forms that have decreased or  
 CC aberrant activity compared to NOVX wild type protein, such as diabetes,  
 CC obesity, metabolic disturbances associated with obesity, anorexia and  
 CC wasting disorders associated with chronic diseases and various cancers,  
 CC infectious diseases and various dyslipidaemias. The nucleic acid  
 CC sequences of the invention may be used in chromosome mapping, identifying  
 CC an individual from minute biological samples (tissue typing), and in  
 CC forensic identification of a biological sample. The present nucleic acid  
 CC sequence encodes a NOVX protein of the invention  
 XX  
 SQ Sequence 10136 BP; 2147 A; 3060 C; 2744 G; 2185 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 10136; DB 6; Length 10136;  
 Query Similarity 100.0%; Pred. No. 0;  
 Matches 10136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GTGTTAACTCAGGTTGGTGTGTCCTCCAGACATATATGTGTCCAGACCTGGCATACC 240  
 DB 181 GTGTTAACTCAGGTTGGTGTGTCCTCCAGACATATATGTGTCCAGACCTGGCATACC 240  
 QY 241 GAAAGGGGCAAAAGCTAGGCTCCGATTTTCAGGTTAGGATCCAGGCTCCAGTTCACTGC 300  
 DB 241 GAAAGGGGCAAAAGCTAGGCTCCGATTTTCAGGTTAGGATCCAGGCTCCAGTTCACTGC 300  
 QY 301 AAGAGGGCTATGACCTGCAAGGGGTCAAGGGGATCACTGTATGAAGTAGAGGACATG 360  
 DB 301 AAGAGGGCTATGACCTGCAAGGGGTCAAGGGGATCACTGTATGAAGTAGAGGACATG 360  
 QY 361 TTGCGGCTGAGGAGGACCAAGGCACTGTGCGAGCCGATGTGTATGATGCCACTT 420  
 DB 361 TTGCGGCTGAGGAGGACCAAGGCACTGTGCGAGCCGATGTGTATGATGCCACTT 420  
 QY 421 CGAGGCCCCCTGGGATCATACCTCCCAATTTCCCAATTTCCCAATTTCCCAATTTCCCA 480  
 DB 421 CGAGGCCCCCTGGGATCATACCTCCCAATTTCCCAATTTCCCAATTTCCCAATTTCCCA 480  
 QY 481 CACTGTGTGTGATCATCAGACCTCAAGCCCTCCAGAGTATCAAGCTGCTGCTTGGAG 540  
 DB 481 CACTGTGTGTGATCATCAGACCTCAAGCCCTCCAGAGTATCAAGCTGCTGCTTGGAG 540  
 QY 541 GAGTTGATTTGGAGAGGGGCTATGACACCTTGAACGCTGATGTGTGTGATGATGGG 600  
 DB 541 GAGTTGATTTGGAGAGGGGCTATGACACCTTGAACGCTGATGTGTGTGATGATGGG 600  
 QY 601 GACCAAGACAGTTCTCTCATATGTCCTCAAAATATGCTGAGTACAGCCCTCCACACCCA 660  
 DB 601 GACCAAGACAGTTCTCTCATATGTCCTCAAAATATGCTGAGTACAGCCCTCCACACCCA 660  
 QY 661 GGCCTTGCCATCCCAAGAGAGATGTCTGGGACATCTGAGGACAAATGATGATCTT 720  
 DB 661 GGCCTTGCCATCCCAAGAGAGATGTCTGGGACATCTGAGGACAAATGATGATCTT 720  
 QY 721 GAGATCTGTGTGATCATTTAGCAGTTGATGATGATGATGATGATGATGATGATGATGAT 780  
 DB 721 GAGATCTGTGTGATCATTTAGCAGTTGATGATGATGATGATGATGATGATGATGATGAT 780  
 QY 781 AAGACTTCTATGCTGTGAACTTTGTTGCTCTGGGACAGAGTCCAGGACAGGCAATGTC 840  
 DB 781 AAGACTTCTATGCTGTGAACTTTGTTGCTCTGGGACAGAGTCCAGGACAGGCAATGTC 840  
 QY 841 GGTGACCTTGACCTTACCTGATATGAGCCGAGGAGGAGGCTCCGCTTTCACACGCTGAC 900  
 DB 841 GGTGACCTTGACCTTACCTGATATGAGCCGAGGAGGAGGCTCCGCTTTCACACGCTGAC 900  
 QY 901 ACACTAAGTTTGAAGTCCAGCCGCTTTGAGCTGTGAGGACAGAGGCAATCAATGTC 960  
 DB 901 ACACTAAGTTTGAAGTCCAGCCGCTTTGAGCTGTGAGGACAGAGGCAATCAATGTC 960  
 QY 961 CAAAGAAATTAACCAATGCTGCTTAAGAAAGCAAGGCTGCTGCTTCTTCTTCAAC 1020  
 DB 961 CAAAGAAATTAACCAATGCTGCTTAAGAAAGCAAGGCTGCTGCTTCTTCTTCAAC 1020  
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 DB 1021 TTACACGACCCGCTGTGGGTTGCTGCTTCCCAATACCAAGAGGATGATGCAACAC 1080  
 QY 1081 CTCACCTGTGTGTGCTATCTTGGGACGCTGAGAGCCGATCACTGACCTTCAAC 1140  
 DB 1081 CTCACCTGTGTGTGCTATCTTGGGACGCTGAGAGCCGATCACTGACCTTCAAC 1140  
 QY 1141 GACATTGAGTGAAGCTTCAATTTGATTTCTGTGTCATCAAGATGAGGACCCGCGAG 1200  
 DB 1141 GACATTGAGTGAAGCTTCAATTTGATTTCTGTGTCATCAAGATGAGGACCCGCGAG 1200  
 QY 1201 GCGCCGCTCTGGGACCTTCTCAGAAACAGCTTCCCTCCATCAACAGAGTGGC 1260  
 DB 1201 GCGCCGCTCTGGGACCTTCTCAGAAACAGCTTCCCTCCATCAACAGAGTGGC 1260  
 QY 1261 CACGTGCGCCGCTGTGAGTTCCAGACTGACCTCACAAGGAGAGGAGGCTTCAACATC 1320

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Db 1261 CACGCGCCCGCTCTCGAGTTCCAGACTGACCACTCCAGAGGAGGGGCTTCAACATC 1320
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Db 1321 ACTTTTACCACTTCCGACACAACAGAGTCCCGGATCTCTGGCTTCAATAATGGCAAA 1380
Qy 1381 CGGTTTGGGGAGCAGCTCCAGCTGAGGAGCTCCATCTCTCTGCTGATGAAGGCTTC 1440
Db 1381 CGGTTTGGGGAGCAGCTCCAGCTGAGGAGCTCCATCTCTCTGCTGATGAAGGCTTC 1440
Qy 1441 CTTGGGACTCAGAGGCTCAGAGACCAATCACTGCTCTGAGAGAGGAGCGCTGCTCG 1500
Db 1441 CTTGGGACTCAGAGGCTCAGAGACCAATCACTGCTCTGAGAGAGGAGCGCTGCTCG 1500
Qy 1501 AACAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 AACAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1561 ACCATCTCTCTCTCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1561 ACCATCTCTCTCTCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
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Db 1621 ATTGAGGCCAGCAGGCTTACCCATCAAAATCACTTGCAGAGATTCAAAACCGAGTTC 1680
Qy 1681 AACTATGACACCTTGGAAGTACGCGATGCGGCGGACTTACTCAGCGCTTGTATCGGGATT 1740
Db 1681 AACTATGACACCTTGGAAGTACGCGATGCGGCGGACTTACTCAGCGCTTGTATCGGGATT 1740
Qy 1741 TACCAAGGGAGCCAGGTTCCAGTTCATCAGACAGCAACTACTCACTCACTCCCTC 1800
Db 1741 TACCAAGGGAGCCAGGTTCCAGTTCATCAGACAGCAACTACTCACTCACTCCCTC 1800
Qy 1801 TTCTCTACCGAAGAGTCACTCGGACATCGGCTTTCAGCTCGCTATGAGACTATAGA 1860
Db 1801 TTCTCTACCGAAGAGTCACTCGGACATCGGCTTTCAGCTCGCTATGAGACTATAGA 1860
Qy 1861 CTGCACTGACCACTGTCTGATCCAGAAATCCAGTAATGAGACGCTCATGGAAT 1920
Db 1861 CTGCACTGACCACTGTCTGATCCAGAAATCCAGTAATGAGACGCTCATGGAAT 1920
Qy 1921 GACTTCTAGTGGGCGCTGAGACTTCACTGAGTCACTCGGCTGCTCACTTAAGTGA 1980
Db 1921 GACTTCTAGTGGGCGCTGAGACTTCACTGAGTCACTCGGCTGCTCACTTAAGTGA 1980
Qy 1981 GGGGAGCCTCTGAGAGTGTAGGCCAACTTCACTGAGAGCGGCGCTGCGCACTTGTGA 2040
Db 1981 GGGGAGCCTCTGAGAGTGTAGGCCAACTTCACTGAGAGCGGCGCTGCGCACTTGTGA 2040
Qy 2041 GCTCTCTGTGTGCTTCACTTAAGGCTCACTGAGGAGCACTTGTGCGCAGGGTTCCCT 2100
Db 2041 GCTCTCTGTGTGCTTCACTTAAGGCTCACTGAGGAGCACTTGTGCGCAGGGTTCCCT 2100
Qy 2101 GACTTCTAACCCAACTTGAATGCACTGAGTGAATGAAACATCTATGAGCAAGGAT 2160
Db 2101 GACTTCTAACCCAACTTGAATGCACTGAGTGAATGAAACATCTATGAGCAAGGAT 2160
Qy 2161 GTGTTCTTCACTTCCACCTTCCACCTGAGAAAGTGGCAGTACCTTCCATCACT 2220
Db 2161 GTGTTCTTCACTTCCACCTTCCACCTGAGAAAGTGGCAGTACCTTCCATCACT 2220
Qy 2221 GAGAAAGGAGCTTCAACCAAGCCCTGAGAGCACTAAGTATCTGAGTGGCCAGCTCC 2280
Db 2221 GAGAAAGGAGCTTCAACCAAGCCCTGAGAGCACTAAGTATCTGAGTGGCCAGCTCC 2280
Qy 2281 ATCAGAGCTGGGCTCTAAGGCACTTCACTGAGTGGCTGGCTTCACTTGAATTTCTCC 2340
Db 2281 ATCAGAGCTGGGCTCTAAGGCACTTCACTGAGTGGCTGGCTTCACTTGAATTTCTCC 2340
Qy 2341 ATGTCATATGAAGATTCAACATCACTTCTCAGATGAGCACTTGAAGCCCTGTGAGAG 2400

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Db 2341 ATGTCATATGAAGATTCAACATCACTTCTCAGATGAGCACTTGAAGCCCTGTGAGAG 2400
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Db 2401 CCGAGAGTCCAGCCTTACAGCATCCGGAAGGGCTTGCAGTTTGGGTGGCGCACCTTG 2460
Qy 2461 ACCTTCTCTGCTTCCCGGATACCGTCTGAGAGGACCGCCGATCACTGCTGAGG 2520
Db 2461 ACCTTCTCTGCTTCCCGGATACCGTCTGAGAGGACCGCCGATCACTGCTGAGG 2520
Qy 2521 GGCAGACGGGCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 2521 GGCAGACGGGCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Qy 2581 GTCAAGAGACTCAGAGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
Db 2581 GTCAAGAGACTCAGAGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
Qy 2641 CATGATGATCTACTCCATCCAGACCCAGCGGAGGGAATTCACTGAGAAAGCCAG 2700
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Qy 2701 GCATTGAACTCTCGAAGAGATGCTCTCAAGTTTATGATGCAACAACCTCGCC 2760
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Db 2761 CGTTTGTGGGAGTTTATGCACTGAGATGAGAGGGGATGAGTGAACAGCAATCC 2820
Qy 2821 AGCAGCTGTGCTGATTTTCACTGATGCTGAGAAACACCAAGCAAGGCTTGAACCTG 2880
Db 2821 AGCAGCTGTGCTGATTTTCACTGATGCTGAGAAACACCAAGCAAGGCTTGAACCTG 2880
Qy 2881 CACTTTTCCAGTTTGAATCATCAATGATGAGAACCCAGAACCCCAAGTTTGCTTAC 2940
Db 2881 CACTTTTCCAGTTTGAATCATCAATGATGAGAACCCAGAACCCCAAGTTTGCTTAC 2940
Qy 2941 AAGTTTCAATGAAAGTATTTTGAAGGAGTCTCGTCTGAGTGAAGGAGGAGGAGGAG 3000
Db 2941 AAGTTTCAATGAAAGTATTTTGAAGGAGTCTCGTCTGAGTGAAGGAGGAGGAGGAG 3000
Qy 3001 TACAGCTGCGGGGATGAGAGAGCTGCTGCTGAGTGAAGGAGGAGGAGGAGGAGGAG 3060
Db 3001 TACAGCTGCGGGGATGAGAGAGCTGCTGCTGAGTGAAGGAGGAGGAGGAGGAGGAG 3060
Qy 3061 CGGCTCTGCGCACTGTGTGCTGCGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 3120
Db 3061 CGGCTCTGCGCACTGTGTGCTGCGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 3120
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Qy 3181 ATGGAAGCAGAGGCGGCTGCACTTGGGCTTCACTTCTGCTGCTGCTGCTGCTGCTG 3240
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Qy 3241 GTTCAAGAGTGTGAGCACTTGGAGTGGGCTGTGAGAGGCGGAGTGTGCTGGAAGAG 3300
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Db 3301 CTGAGTGGGCGGCGCTGCGCAAGGACCTGCACTTGAAGGAGGAGGAGGAGGAGGAG 3360
Qy 3361 TTCAAGACTGACTTCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
Db 3361 TTCAAGACTGACTTCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
Qy 3421 GCAAGTCTGTGAAATGACCTTGGAGTCCCGCAAGATGGAGTCCGAGTGGTGAAGTTGG 3480
Db 3421 GCAAGTCTGTGAAATGACCTTGGAGTCCCGCAAGATGGAGTCCGAGTGGTGAAGTTGG 3480

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QY	3481	GAACCGGCGACCTCCACAGTGTTCACAGTGAACCCCTGACTACGGCTGCAGGGAAAGTGA	3540
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QY	3541	GAGATCAGCTGTGTGAAGATCGAGAACAGGTTCTTCTGGCAGCCCGCCACATGC	3600
Db	3541	GAGATCAGCTGTGTGAAGATCGAGAACAGGTTCTTCTGGCAGCCCGCCACATGC	3600
QY	3601	ATGCCTCCCTGGGGGGAGACTTACACAGAACATCTGGAAGTCACTCTACCAAAATTAC	3660
Db	3601	ATGCCTCCCTGGGGGGAGACTTACACAGAACATCTGGAAGTCACTCTACCAAAATTAC	3660
QY	3661	CCAGAACCTTACCCGCGCAGGCGAAAGAGTGTGACTGGAAGTGAACCGTCTGACACGACTAC	3720
Db	3661	CCAGAACCTTACCCGCGCAGGCGAAAGAGTGTGACTGGAAGTGAACCGTCTGACACGACTAC	3720
QY	3721	GTCAATCGCCCTGTGATTTAAATCATCTTTAACTGGAGCTGGCTATGACTCTCTCCATATC	3780
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QY	3781	TACGACGAGCGGAGCTCTCTCAGCCCTCTCATAGAAAGCTTATAGACTCCACAGTCCCA	3840
Db	3781	TACGACGAGCGGAGCTCTCTCAGCCCTCTCATAGAAAGCTTATAGACTCCACAGTCCCA	3840
QY	3841	GGCCGCATTTGAAGCAGCAGCAAGCTCTTCTCGCTTCGCGACGATGACTCTGTG	3900
Db	3841	GGCCGCATTTGAAGCAGCAGCAAGCTCTTCTCGCTTCGCGACGATGACTCTGTG	3900
QY	3901	AGCAATGCTGGCTTCGTATATGACATATACAAAAAACCGGGGAGTACATGTTTGAATCCT	3960
Db	3901	AGCAATGCTGGCTTCGTATATGACATATACAAAAAACCGGGGAGTACATGTTTGAATCCT	3960
QY	3961	GGTTCATCATGAAGAACGGACACAGGGTGGGGTCCGACCTGAAGCTGGGCTCTCCGTACCC	4020
Db	3961	GGTTCATCATGAAGAACGGACACAGGGTGGGGTCCGACCTGAAGCTGGGCTCTCCGTACCC	4020
QY	4021	TACTACTGCCACGGGGGCTACGAAATTAGGGCACCTTGACCTTGAGTGTGATCTTGGGG	4080
Db	4021	TACTACTGCCACGGGGGCTACGAAATTAGGGCACCTTGAGCTTGAGTGTGATCTTGGGG	4080
QY	4081	CCTGATGGGAAGCCCGTGTGGAAACAATCCCGGCGAGTCTGCACAGCCCTCTGTGGAGGA	4140
Db	4081	CCTGATGGGAAGCCCGTGTGGAAACAATCCCGGCGAGTCTGCACAGCCCTCTGTGGAGGA	4140
QY	4141	CAGTATGTGGGTTGGGACGAGGTGTCTTGTCTCCCAATACACCCCGAAGTCAACAAGT	4200
Db	4141	CAGTATGTGGGTTGGGACGAGGTGTCTTGTCTCCCAATACACCCCGAAGTCAACAAGT	4200
QY	4201	GGACGATCTGTGTATTTTGTATCTGTGGCCCAAGGACTATGTGTGTGTGGCAAGTTTC	4260
Db	4201	GGACGATCTGTGTATTTTGTATCTGTGGCCCAAGGACTATGTGTGTGTGGCAAGTTTC	4260
QY	4261	GCTTCTTTCACACGGCCCTCAACAAGCTGTGTGAGTTCGACAGGCGCACAGCACAC	4320
Db	4261	GCTTCTTTCACACGGCCCTCAACAAGCTGTGTGAGTTCGACAGGCGCACAGCACAC	4320
QY	4321	TGCGGGCTCTCTACGTTCTCTCTCTCGGGCTCCCATACAGGAATCATCTGCTTGGCCACC	4380
Db	4321	TGCGGGCTCTCTACGTTCTCTCTCTCGGGCTCCCATACAGGAATCATCTGCTTGGCCACC	4380
QY	4381	TCCATTCAAAGTTCTATTAAAGTTCAGGCGCAAAAGGCTCTGCACAGCCAGAGGCTTCCAC	4440
Db	4381	TCCATTCAAAGTTCTATTAAAGTTCAGGCGCAAAAGGCTCTGCACAGCCAGAGGCTTCCAC	4440
QY	4441	TTTGTCTACCAAGCGGTTCTTGAAACAAGCGCACAGTCAAGTCAAGTCTGTGCCGAAACC	4500
Db	4441	TTTGTCTACCAAGCGGTTCTTGAAACAAGCGCACAGTCAAGTCAAGTCTGTGCCGAAACC	4500
QY	4501	CGCTATGGCAAGAGGCTGGGCGATGACATTCCTCGGTGGGGGCGCATGTCCGTTTGAATGC	4560
Db	4501	CGCTATGGCAAGAGGCTGGGCGATGACATTCCTCGGTGGGGGCGCATGTCCGTTTGAATGC	4560

QY	4561	AACCTCGGCGATGCGCTGACGGGGAGTGGCCAGAGATGAGATGCGCTCCTGTGCTGTGGAGGC	4520
Db	4561	AACCTCGGCGATGCGCTGACGGGGAGTGGCCAGAGATGAGATGCGCTCCTGTGCTGTGGAGGC	4520
QY	4621	TTGGCCCAATGGAAATGCTCAGCGCCCACTGTGTGTGTGCTGTGTGAGGCAACTTCACA	4680
Db	4621	TTGGCCCAATGGAAATGCTCAGGCGCCCACTGTGTGTGTGCTGTGTGAGGCAACTTCACA	4680
QY	4681	GAGCGCAGGGGACACATCCTGTGCTCCCTGGCTTCCAGAGCCGTATCTTCAACAGCCTTCAAC	4740
Db	4681	GAGCGCAGGGGACACATCCTGTGCTCCCTGGCTTCCAGAGCCGTATCTTCAACAGCCTTCAAC	4740
QY	4741	TGTGTGTGGAAAGATCGTGTGTCCTCCCGAAGGGCGCTGGGATCCAGATCCCAAGTTTGCAGTTT	4800
Db	4741	TGTGTGTGGAAAGATCGTGTGTCCTCCCGAAGGGCGCTGGGATCCAGATCCCAAGTTTGCAGTTT	4800
QY	4801	GTGACAGAGCAGAACTGTGGACTCGCTGGAAAGTATTTGATGTGTCCAGATTAACACTGTAAAC	4860
Db	4801	GTGACAGAGCAGAACTGTGGACTCGCTGGAAAGTATTTGATGTGTCCAGATTAACACTGTAAAC	4860
QY	4861	ATGCTGGGGAGTTTCTCAGGAAACAACGCTGCTCCCTTCTGAAACAGCACTTCCAACAG	4920
Db	4861	ATGCTGGGGAGTTTCTCAGGAAACAACGCTGCTCCCTTCTGAAACAGCACTTCCAACAG	4920
QY	4921	CTTCACTTCAATTTCTATCTCAGATATCAGGATATCTGCACCTGAGCTTCCACTTGGAGTAC	4980
Db	4921	CTTCACTTCAATTTCTATCTCAGATATCAGGATATCTGCACCTGAGCTTCCACTTGGAGTAC	4980
QY	4981	AAACCGTGTGGCCCTGACAGATTGTCCGGAACTGTGTGCCCCAGTAACTGCGGGGTGAAGACT	5040
Db	4981	AAACCGTGTGGCCCTGACAGATTGTCCGGAACTGTGTGCCCCAGTAACTGCGGGGTGAAGACT	5040
QY	5041	GGCGAGCGCTATCTTGTGTGAATGATGTGTGTCTTTCCAGTGTGAGCCGGGATATGCTCTC	5100
Db	5041	GGCGAGCGCTATCTTGTGTGAATGATGTGTGTCTTTCCAGTGTGAGCCGGGATATGCTCTC	5100
QY	5101	CAGGGCCACGCGCCACATCTCCTGTGATGCCGGAAACAATGGGGCGATGGAACTACCCCTCT	5160
Db	5101	CAGGGCCACGCGCCACATCTCCTGTGATGCCGGAAACAATGGGGCGATGGAACTACCCCTCT	5160
QY	5161	CCACTCTGTATTGACAGATGTGGGGGAAACAGTGGAGGAGATGAGAGGGGATGATCCTGAGC	5220
Db	5161	CCACTCTGTATTGACAGATGTGGGGGAAACAGTGGAGGAGATGAGAGGGGATGATCCTGAGC	5220
QY	5221	CCCGGCTTCCAGGCAACTACCCCAATGATGATGAGCTGTCTCTGGAAATATAGCACTGCCC	5280
Db	5221	CCCGGCTTCCAGGCAACTACCCCAATGATGATGAGCTGTCTCTGGAAATATAGCACTGCCC	5280
QY	5281	GTGGGCTTTGGAAGCTCAATCCAGTTCTCTAATCTTCCACCGAGGCCCAACAGACTAC	5340
Db	5281	GTGGGCTTTGGAAGCTCAATCCAGTTCTCTAATCTTCCACCGAGGCCCAACAGACTAC	5340
QY	5341	ATTAGAAATCCGGAATGAGCCCTATGAGACAGCCGCACTGATGTGGAAAGATTCACTGAGAGC	5400
Db	5341	ATTAGAAATCCGGAATGAGCCCTATGAGACAGCCGCACTGATGTGGAAAGATTCACTGAGAGC	5400
QY	5401	GAGCTTCCAAAGCTCCTCTCTCTCCAGCTCCCAAGACACACCGTGTATTTTCCACAGGAC	5460
Db	5401	GAGCTTCCAAAGCTCCTCTCTCTCCAGCTCCCAAGACACACCGTGTATTTTCCACAGGAC	5460
QY	5461	CACCTCCCAAGATTCGGCCAGATTAACTGTGAGATATCAGGCTATGTGAACCTTCAAGAGTGC	5520
Db	5461	CACCTCCCAAGATTCGGCCAGATTAACTGTGAGATATCAGGCTATGTGAACCTTCAAGAGTGC	5520
QY	5521	CCAGACCCAGAGCCCTTGGCCCAATGGGATTTGTGAGGGAGCTGTGCTCAACGTTGGGACAA	5580
Db	5521	CCAGACCCAGAGCCCTTGGCCCAATGGGATTTGTGAGGGAGCTGTGCTCAACGTTGGGACAA	5580
QY	5581	TCAGTGACCTTGAAGTGTCTCCCGGGGTATCAATTTGACTGGCCACCTGTCTTCAAGTGT	5640
Db	5581	TCAGTGACCTTGAAGTGTCTCCCGGGGTATCAATTTGACTGGCCACCTGTCTTCAAGTGT	5640
QY	5641	CAACATGGCACCAACCGGAATGGGACACACCCCTGCCCAAGTGTGAATGCCCTTGTGTGC	5700



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Db 5701 GGGAAATACATCTTCCCAACGGCACTGTGTACTCCCGGGGTCCCTGACCCGTATCCG 5760  
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DB 3781 TACAGGAGGAGGAGCTCTTCAAGCCCTCTCATATGAAAGTCTTATGAGTCTTCAAC 3840  
QY 3841 GGGCGATTTGAAGAGCAGCAGCAAGCCCTCTTCTGAGCTTCCGAGGAGTGAATGTG 3900  
DB 3841 GGGCGATTTGAAGAGCAGCAGCAAGCCCTCTTCTGAGCTTCCGAGGAGTGAATGTG 3900  
QY 3901 AGCAATGCTGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960  
DB 3901 AGCAATGCTGCTGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960  
QY 3961 GGTTCATCAAGAGCAGCAGCAGGAGTGGGCTTCAAGTGGGCTTCTTCTGAGTCC 4020  
DB 3961 GGTTCATCAAGAGCAGCAGCAGGAGTGGGCTTCAAGTGGGCTTCTTCTGAGTCC 4020  
QY 4021 TACTACTGCAAGGGGCTTCAAGAGTGGGAGCACTTGAAGTGGGCTTCAAGTGGGAG 4080  
DB 4021 TACTACTGCAAGGGGCTTCAAGAGTGGGAGCACTTGAAGTGGGCTTCAAGTGGGAG 4080  
QY 4081 CCTGATGAGAGACCCGCTGTGGAACAATCCCGGAGCTTGTGCAAGAGCCCTGTGGGGA 4140  
DB 4081 CCTGATGAGAGACCCGCTGTGGAACAATCCCGGAGCTTGTGCAAGAGCCCTGTGGGGA 4140  
QY 4141 CAGTATGTGGTTCGAGCGAGTGTGCTTGTCCCACTTACCCAGAACTTACAGT 4200  
DB 4141 CAGTATGTGGTTCGAGCGAGTGTGCTTGTCCCACTTACCCAGAACTTACAGT 4200  
QY 4201 GGAAGATGTGCTTGTATTTTGTATCTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTG 4260  
DB 4201 GGAAGATGTGCTTGTATTTTGTATCTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTG 4260  
QY 4261 GCTTCTTCAACAGGCGCTTCAAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4320

D	b		4261	GCTTCTTTCAACAGGCGCCCTCAACAGATGTGGTAGGTTACACAGCGGCCAACAGCAGCAC	4320
O	y		4321	TGGGCGCTCTCAGACTCCCTCTCGGCGCTCCCATACAGAGAAATCATCTGCCTTGCCACC	4380
D	b		4321	TGGCGGCTCTCAGACTCCCTCTCGGCGCTCCCATACAGAGAAATCATCTGCCTTGCCACC	4380
O	y		4381	TCGAATCAAAGTTCATTAAATTTAAGGCGCCAAAGGCTCCGACAGGCGAGAGGTTTCAC	4440
D	b		4381	TCGAATCAAAGTTCATTAAATTTAAGGCGCCAAAGGCTCCGACAGGCGAGAGGTTTCAC	4440
O	y		4441	TTTGTCTACCAAGCGGTTCTCTGAAACAAGCCCAACGAGTGCAGCTCTGTGCCGAACCC	4500
D	b		4441	TTTGTCTACCAAGCGGTTCTCTGAAACAAGCCCAACGAGTGCAGCTCTGTGCCGAACCC	4500
O	y		4501	CGCTATGGCAAGAAGCTGGGCGAGTACTTCTCGGTGGGGGCATTCGTCCTTCGATATGC	4560
D	b		4501	CGCTATGGCAAGAAGCTGGGCGAGTACTTCTCGGTGGGGGCATTCGTCCTTCGATATGC	4560
O	y		4561	AACCTCGGCTATGCCCTCAGGGGTCGCGACAGATCCAGATGCCTCCCTGTGCCCTGGGGCC	4620
D	b		4561	AACCTCGGCTATGCCCTCAGGGGTCGCGACAGATCCAGATGCCTCCCTGTGCCCTGGGGCC	4620
O	y		4621	TTGGCCCAATGGAATGTCTCAGCGCCACGTTGTGGTGGCGGTGAGAGGCMACTTACA	4680
D	b		4621	TTGGCCCAATGGAATGTCTCAGCGCCACGTTGTGGTGGCGGTGAGAGGCMACTTACA	4680
O	y		4681	GAGGCGAAGGGGACCATCTGTGCCCTGAGCTCCAGAGCGGTACCTCAACAGGCTCAAC	4740
D	b		4681	GAGGCGAAGGGGACCATCTGTGCCCTGAGCTCCAGAGCGGTACCTCAACAGGCTCAAC	4740
O	y		4741	TGTGTGTGAAGATGTGTGTCCCAGAGGCGGTGACATCCAGATCCAAATTGTCAATTTT	4800
D	b		4741	TGTGTGTGAAGATGTGTGTCCCAGAGGCGGTGACATCCAGATCCAAATTGTCAATTTT	4800
O	y		4801	GTGAAGAAGCAAACTGGGACTCGCTGGAAATAATTGATGGCAGATAACACTGTATAC	4860
D	b		4801	GTGAAGAAGCAAACTGGGACTCGCTGGAAATAATTGATGGCAGATAACACTGTATAC	4860
O	y		4861	ATGCTGGGGAAGTTTCTCAAGAACAAACGTGCCTGCCCTTGTAAACAGCACTCCAACGAG	4920
D	b		4861	ATGCTGGGGAAGTTTCTCAAGAACAAACGTGCCTGCCCTTGTAAACAGCACTCCAACGAG	4920
O	y		4921	CTCTACCTTCAATTTTCACTCAAGATTCAGACCGATTCGAGCTGATCCATTGGAATAC	4980
D	b		4921	CTCTACCTTCAATTTTCACTCAAGATTCAGACCGATTCGAGCTGATCCATTGGAATAC	4980
O	y		4981	AAAAAGGTGGGCTCAGCAGATTTGTCGGAAACCTGCTGTGCCAGATTAACGGGGTGAAGCT	5040
D	b		4981	AAAAAGGTGGGCTCAGCAGATTTGTCGGAAACCTGCTGTGCCAGATTAACGGGGTGAAGCT	5040
O	y		5041	GGCGAGCGCTACTTGTGTGATATATGTGTCTTTCCAGTGTAGCCGGGATATGCCCC	5100
D	b		5041	GGCGAGCGCTACTTGTGTGATATATGTGTCTTTCCAGTGTAGCCGGGATATGCCCC	5100
O	y		5101	CAGGCGCAAGCCCAATCTCTGCAATGCCGGAACAGTGGCGGATGGAATCACTACCTCT	5160
D	b		5101	CAGGCGCAAGCCCAATCTCTGCAATGCCGGAACAGTGGCGGATGGAATCACTACCTCT	5160
O	y		5161	CCACTCTGTATTGCAACAGTGTGGGGGAAACGTGAGAGATGAGAGGGGTATCTCTGAGC	5220
D	b		5161	CCACTCTGTATTGCAACAGTGTGGGGGAAACGTGAGAGATGAGAGGGGTATCTCTGAGC	5220
O	y		5221	CCCGGTTCCAGGGAACBACCCCAAGTAAACATGAGCTGCTCTGAAAATATGACTGCC	5280
D	b		5221	CCCGGTTCCAGGGAACBACCCCAAGTAAACATGAGCTGCTCTGAAAATATGACTGCC	5280
O	y		5281	GTGGGCTTTGAGACTCAATCCAGTTCTCGAACTTTCACCCGAGCCCAACGACATAC	5340
D	b		5281	GTGGGCTTTGAGACTCAATCCAGTTCTCGAACTTTCACCCGAGCCCAACGACATAC	5340
O	y		5341	ATAGAAATCCGGAATGGCCCTATGAGACCAAGCCGATGATGGGAAGATTCAATGGGAAGC	5400
D	b		5341	ATAGAAATCCGGAATGGCCCTATGAGACCAAGCCGATGATGGGAAGATTCAATGGGAAGC	5400

Qy	5401	GAGCTTCCAACTCCCTCTCTTCCAGCTCCCAAGAGCAACCCGTATTTTCCACAGGAC	5460
Db	5401	GAGCTTCCAACTCCCTCTCTTCCAGCTCCCAAGAGCAACCCGTATTTTCCACAGGAC	5460
Qy	5461	CACCTCCAGATCGGACAGATTCAACTGGAGTATAGGCTTATGAATCTTCAAGATGC	5520
Db	5461	CACCTCCAGATTCGGCCAGATTTCACTGGAGTATAGGCTTATGAATCTTCAAGATGC	5520
Qy	5521	CCAGACCCAGAGCCCTTTGGCCATGCGATTGTGAGGGGAGCTGGCTTCAACTGTGGACAA	5580
Db	5521	CCAGACCCAGAGCCCTTTGGCCATGCGATTGTGAGGGGAGCTGGCTTCAACTGTGGACAA	5580
Qy	5581	TCAGGACCTTCGAGTGCCTCCGGGGGATCAATTGACTGGACACCTGTCTCTCACTGT	5640
Db	5581	TCAGGACCTTCGAGTGCCTCCGGGGATCAATTGACTGGACACCTGTCTCTCACTGT	5640
Qy	5641	CAACATGGCACCAACCGGAACTGGGACACCCCTGCTCCAAGTGTGAAGTCCCTTGTGGC	5700
Db	5641	CAACATGGCACCAACCGGAACTGGGACACCCCTGCTCCAAGTGTGAAGTCCCTTGTGGC	5700
Qy	5701	GGGAAATCATCTTCTTCCACGGCACTGTATACCCCGGGGTCCCTAGCCGCTACTCC	5760
Db	5701	GGGAAATCATCTTCTTCCACGGCACTGTATACCCCGGGGTCCCTAGCCGCTACTCC	5760
Qy	5761	AGCTCCAGAGCTGTGTGTGGCTGATCAACCGTGCCTATGGCCATGGCGGTCCGCTCAAC	5820
Db	5761	AGCTCCAGAGCTGTGTGTGGCTGATCAACCGTGCCTATGGCCATGGCGGTCCGCTCAAC	5820
Qy	5821	CTCAGCTGTGTGCAGACAGAGCCCTCTGGAGATTTTCATCACTCTGGAGTGGCCACAG	5880
Db	5821	CTCAGCTGTGTGCAGACAGAGCCCTCTGGAGATTTTCATCACTCTGGAGTGGCCACAG	5880
Qy	5881	CAAAAGACCAACCGGCTCGGCGTCTTCAACCGGAGCATGGCCAAAGAAACGTGCAGGT	5940
Db	5881	CAAAAGACCAACCGGCTCGGCGTCTTCAACCGGAGCATGGCCAAAGAAACGTGCAGGT	5940
Qy	5941	TCATCCAAACAGGTCTGTCAAGTTCCACCGTATGACGCCAAGGGGGATCTTGGC	6000
Db	5941	TCATCCAAACAGGTCTGTCAAGTTCCACCGTATGACGCCAAGGGGGATCTTGGC	6000
Qy	6001	AATGCTTCTCCGCTTATCCACTCAACCAAGGCCCTCTCCACCATCTTCCCAAGCC	6060
Db	6001	AATGCTTCTCCGCTTATCCACTCAACCAAGGCCCTCTCCACCATCTTCCCAAGCC	6060
Qy	6061	GAACTGTCAACAGATGAAGATTCATATAGTGATCATCGTACGTACAGATGCTC	6120
Db	6061	GAACTGTCAACAGATGAAGATTCATATAGTGATCATCGTACGTACAGATGCTC	6120
Qy	6121	CCTGGCTTACTTATGTGGGGATGAAATTTCTGACCTGCAAACTTGGAACTTACTGGAG	6180
Db	6121	CCTGGCTTACTTATGTGGGGATGAAATTTCTGACCTGCAAACTTGGAACTTACTGGAG	6180
Qy	6181	TTTGAAGGACCAACCCCGATATGTGAATGACCTGTCCAAACAAATGACCTTCTGCACAC	6240
Db	6181	TTTGAAGGACCAACCCCGATATGTGAATGACCTGTCCAAACAAATGACCTTCTGCACAC	6240
Qy	6241	TCACAGGCGTGATCTTGAAGCAAGCTACCTTGAAGCTATCCCACTTCCAGACTGCG	6300
Db	6241	TCACAGGCGTGATCTTGAAGCAAGCTACCTTGAAGCTATCCCACTTCCAGACTGCG	6300
Qy	6301	TCCTGGCTGTGAGTGGAGCCGACCTATTAACATCTCCCTCAACAGTGAATCTTCTC	6360
Db	6301	TCCTGGCTGTGAGTGGAGCCGACCTATTAACATCTCCCTCAACAGTGAATCTTCTC	6360
Qy	6361	AGGAGAGACATATGATAGTTTGAATTTTGAATGTATCAATCAAGACAGAGTCTCTG	6420
Db	6361	AGGAGAGACATATGATAGTTTGAATTTTGAATGTATCAATCAAGACAGAGTCTCTG	6420
Qy	6421	CTGAAAAGCCCTCAGTGGGAATTAATCAAGTCCCTGATTTGTCAACAGCTCAAGAACTCT	6480
Db	6421	CTGAAAAGCCCTCAGTGGGAATTAATCAAGTCCCTGATTTGTCAACAGCTCAAGAACTCT	6480



QY 6481 GTGTACTGCGTTGTCATCTGATCAAGCCTACATCGAAGGCGTTCAAGATCCGCTAT 6540  
Db 6481 GTGTACTGCGTTGTCATCTGATCAAGCCTACATCGAAGGCGTTCAAGATCCGCTAT 6540  
QY 6541 TCAGCCCCCTTACAGCACTGCTCCCAAGGAGCTCACTCATGAGTTTCACTTCAAGCCAGACC 6600  
Db 6541 TCAGCCCCCTTACAGCACTGCTCCCAAGGAGCTCACTCATGAGTTTCACTTCAAGCCAGACC 6600  
QY 6601 AGCACCAGCGCGGAGGCTCCATTCACCTTTGGCTGCAAGCGCGGCTACCGGCTGAGGAG 6660  
Db 6601 AGCACCAGCGCGGAGGCTCCATTCACCTTTGGCTGCAAGCGCGGCTACCGGCTGAGGAG 6660  
QY 6661 CACAGCATGCGCATCTGTACCCGCAACCCCAAGGCTACCACTGTGAGAGCAAGCATC 6720  
Db 6661 CACAGCATGCGCATCTGTACCCGCAACCCCAAGGCTACCACTGTGAGAGCAAGCATC 6720  
QY 6721 CCTCTCTGTACACTCTTTCTGTGGGCTTCTGAGGCTCCCAAGAAATGGAATGTTGTTT 6780  
Db 6721 CCTCTCTGTACACTCTTTCTGTGGGCTTCTGAGGCTCCCAAGAAATGGAATGTTGTTT 6780  
QY 6781 GGCAGAGATGACACAGTGGGAAACCAAGGCGGTGTAACAGTGAAGGCTACCACTC 6840  
Db 6781 GGCAGAGATGACACAGTGGGAAACCAAGGCGGTGTAACAGTGAAGGCTACCACTC 6840  
QY 6841 CAGGACAGCGCTGAGGCACTGCAAGTGTCTGGAACAAGGCTTATGAGCAACCGCAT 6900  
Db 6841 CAGGACAGCGCTGAGGCACTGCAAGTGTCTGGAACAAGGCTTATGAGCAACCGCAT 6900  
QY 6901 GTCCCAACACAGTGTCTCTGTGACTTGTCTGATGTCTGATGCAATCAGGCTGAGCAT 6960  
Db 6901 GTCCCAACACAGTGTCTCTGTGACTTGTCTGATGTCTGATGCAATCAGGCTGAGCAT 6960  
QY 6961 GGCAGATGAGGCTTATCTTTGAGACACAGTATCAGTCCAGGCGGAGGCTGATGCTATC 7020  
Db 6961 GGCAGATGAGGCTTATCTTTGAGACACAGTATCAGTCCAGGCGGAGGCTGATGCTATC 7020  
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Db 7081 TGGAGCTCGGGGACTCTACGCCCACTGCGCAATCATCTCTGTGAGAGCTCCGAT 7140  
QY 7141 CCCCCCAATGSCCAACCGCATCGGAAACATGTCCTGCTACCGGGCAACAGCATCTTCTCC 7200  
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QY 7201 TGCATTTCCGATACACACTGTGTGGCTCCAGGAGTGTGATGTCATGAGGCAATGAGGCTC 7260  
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QY 7261 TGGAGTGGCTCTGAGAGTCCGCTGCTGCTGAGCACTGTGAGCACTCTGAGCCATTTGTC 7320  
Db 7261 TGGAGTGGCTCTGAGAGTCCGCTGCTGCTGAGCACTGTGAGCACTCTGAGCCATTTGTC 7320  
QY 7321 AACGACACATCAATGAGGAGAACTACAGTACCGGGGAGTGTGATACCAATGATCAT 7380  
Db 7321 AACGACACATCAATGAGGAGAACTACAGTACCGGGGAGTGTGATACCAATGATCAT 7380  
QY 7381 GCTGAGTTCGCTGATCGGATGTCTGTGCGCATCTGCGAGAGATCATCTGTGTG 7440  
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QY 7441 GGCAGAACCCCTTTCTGTGTGCAATTAACCTGTGACACCCAGGCAACCTGTCAACGCG 7500  
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QY 7501 CTCACCTCAGGGTAAACAGTTTAACTCAACGATGTGTGCAAGTTTGTGCAACCTGTGG 7560  
Db 7501 CTCACCTCAGGGTAAACAGTTTAACTCAACGATGTGTGCAAGTTTGTGCAACCTGTGG 7560  
QY 7561 TATATGCTGAGGAGGCTGCTAGGTCCCAATGCTGCGGCAAGCGGCAATGAGTGAATG 7620

Db 7561 TATATGCTGAGGAGGCTGCTAGGTCCCAATGCTGCGGCAATGAGTGAATG 7620  
QY 7621 CTGCCCACTGCAAGATCATCACTGTACAGATCTTGTGACACCAAGAAATAGTGTGCT 7680  
Db 7621 CTGCCCACTGCAAGATCATCACTGTACAGATCTTGTGACACCAAGAAATAGTGTGCT 7680  
QY 7681 CAGGTCCAGGCAAGGAGGCGGCAAGGTTCAAGTTGAGGAGCACTGTGTCTTACCGGATG 7740  
Db 7681 CAGGTCCAGGCAAGGAGGCGGCAAGGTTCAAGTTGAGGAGCACTGTGTCTTACCGGATG 7740  
QY 7741 AACCAAGGCTTCTACTCTCTGTGAGCAACCCAGTGTCTGAGTGCAGGAGATGAGCATG 7800  
Db 7741 AACCAAGGCTTCTACTCTCTGTGAGCAACCCAGTGTCTGAGTGCAGGAGATGAGCATG 7800  
QY 7801 GACCGTCCCGGCGGCAAGTGTCTTGTGTGTCTGTGTGCAATCCGAGGCTCCCGCTCAC 7860  
Db 7801 GACCGTCCCGGCGGCAAGTGTCTTGTGTGTCTGTGTGCAATCCGAGGCTCCCGCTCAC 7860  
QY 7861 TCCAGATGTCTGAGACAGTTATACCTGTGAGGAGAGTGTGAGTGAAGCTGATCGGC 7920  
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QY 7921 AAGCGTACTCTGTGTGAGAAACAGCAACCCGATGTGTGTGAGTGAAGTGAAGTGAAG 7980  
Db 7921 AAGCGTACTCTGTGTGAGAAACAGCAACCCGATGTGTGTGAGTGAAGTGAAGTGAAG 7980  
QY 7981 TCCCTCTCTCACTGCTCAGAAACCAAGCTGTGAGTGTGTGAGTGTGTGAGTGTGTG 8040  
Db 7981 TCCCTCTCTCACTGCTCAGAAACCAAGCTGTGAGTGTGTGAGTGTGTGAGTGTGTG 8040  
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Db 8041 CATGCGATCGTTTGGGAGGAGAGCTTGTATCCAGGCACTGTATGAGGCTTCAAGTGTGA 8100  
QY 8101 GCTGCGACAGTGTCTCGGGAGTGTGAGAGCAGCAGCTGTCAAGCAATGCTGTGAGAC 8160  
Db 8101 GCTGCGACAGTGTCTCGGGAGTGTGAGAGCAGCAGCTGTCAAGCAATGCTGTGAGAC 8160  
QY 8161 GGTGCGACAGTGTGTGAGTGTGATCTCTTGTGGAACCTGTGAGCTTCAAGTATATGTC 8220  
Db 8161 GGTGCGACAGTGTGTGAGTGTGATCTCTTGTGGAACCTGTGAGCTTCAAGTATATGTC 8220  
QY 8221 CGAGTTGTGTGAGTGTGAGTGTGATCTCTGAGTGTGTGAGTGTGTGAGTGTGTG 8280  
Db 8221 CGAGTTGTGTGAGTGTGAGTGTGATCTCTGAGTGTGTGAGTGTGTGAGTGTGTG 8280  
QY 8281 GGTATCTACGCAAGGCTGTGCTCAGCCGTCACTGCTCGTCAATGTGTCTGTGACAGGC 8340  
Db 8281 GGTATCTACGCAAGGCTGTGCTCAGCCGTCACTGCTCGTCAATGTGTCTGTGACAGGC 8340  
QY 8341 AGTGAACCTGAGTGTGTGTATTAACCTGTGTGACCTGTGAGTGTGTGAGTGTGTG 8400  
Db 8341 AGTGAACCTGAGTGTGTGTATTAACCTGTGTGACCTGTGAGTGTGTGAGTGTGTG 8400  
QY 8401 CGGCTGTGAGT 8460  
Db 8401 CGGCTGTGAGT 8460  
QY 8461 ATGATGAGT 8520  
Db 8461 ATGATGAGT 8520  
QY 8521 ACCAAGCCGCTGTGAAAGCTCTCATGTGAGGAGCAACCTGCTCATCCCAATGAGGAG 8580  
Db 8521 ACCAAGCCGCTGTGAAAGCTCTCATGTGAGGAGCAACCTGCTCATCCCAATGAGGAG 8580  
QY 8581 GT 8640  
Db 8581 GT 8640  
QY 8641 CAGCTCTCCCTGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8700





PR	11-JUN-2002	2002US-0387836P
PR	11-JUN-2002	2002US-0387859P
PR	12-JUN-2002	2002US-0387933P
PR	12-JUN-2002	2002US-0387934P
PR	12-JUN-2002	2002US-0387966P
PR	12-JUN-2002	2002US-0388022P
PR	12-JUN-2002	2002US-0388056P
PR	13-JUN-2002	2002US-0389123P
PR	14-JUN-2002	2002US-0389118P
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PR	14-JUN-2002	2002US-0389144P
PR	14-JUN-2002	2002US-0389146P
PR	17-JUN-2002	2002US-0389729P
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PR	18-JUN-2002	2002US-0389844P
PR	19-JUN-2002	2002US-0390006P
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PR	17-JUL-2002	2002US-0396706P
PR	06-AUG-2002	2002US-0401628P
PR	09-AUG-2002	2002US-0402156P
PR	09-AUG-2002	2002US-0402256P
PR	09-AUG-2002	2002US-0402389P
PR	12-AUG-2002	2002US-0402786P
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PR	23-SEP-2002	2002US-0412731P
PR	30-SEP-2002	2002US-0414801P
PR	30-SEP-2002	2002US-0414839P
PR	30-SEP-2002	2002US-0414840P
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PR	28-OCT-2002	2002US-0421156P
PR	31-OCT-2002	2002US-0422690P
PR	01-NOV-2002	2002US-0423130P
PR	05-NOV-2002	2002US-0423798P
PR	12-NOV-2002	2002US-0425453P

PI Alsbroek JP, Alvarez E, Anderson DM, Boldo FL, Casman SJ;  
PI Catterton E, Chappoval A, Crabtree-Bokor JR, Edinger SR, Ellemann K;  
PI Erteneburg S, Gangolli EA, Getlach VL, Gorman L, Gunther E, Guo X;  
PI Guev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;  
PI Macleachlan T, Malayankar UM, Mezlok AJ, Millet I, Mishra VS;  
PI Padigan M, Patutarajan M, Pena CE, Peyman JA, Raha D, Rastellil L;  
PI Rieger DK, Rothenberg ME, SCORE P, Shenoy SG, Shinkets RA;  
PI Smithson G, Spleek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;  
PI Zhong H;  
XX  
XX WPI: 2004-081935/08.  
DR P-PSDB; ADH71166.  
DR  
XX  
XX  
PT New NOX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
XX

Example 4, SEQ ID NO 61, 1880bp, English.

Query Match	Similarity	100.0%	Score 10134.4	DB 12	Length 10136
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Qy	1	ATGGCGGGCGCCCCCTCCCGGCGCTTGCCTGCTCCCTTGGCAGTTTGAATTCAGACTGCTCT	60		
Db	1	ATGGCGGGCGCGCCCTCCCGGCGCTTGCCTGCTCCCTTGGCAGTTTGAATTCAGACTGCTCT	60		
Qy	61	GCTTGCATCAGGCACTCCGTGGGGGTGAGACCTCCGAGCTTAAAGCAAAATT	120		
Db	61	GCTTGCATCAGGCACTCCGTGGGGGTGAGACCTCCGAGCTTAAAGCAAAATT	120		
Qy	121	GAGTTGAAGTCTGAGGCTGTAAGCTGATGSCCAGCAAAACAACAGCCAGAAAGCTCT	180		
Db	121	GAGTTGAAGTCTGAGGCTGTAAGCTGATGSCCAGCAAAACAACAGCCAGAAAGCTCT	180		
Qy	181	GTGTTAACTCAGGTTGGTGTGTCCAAAGCATATATATGTGTCCAGACCCTGGCATACC	240		
Db	181	GTGTTAACTCAGGTTGGTGTGTCCAAAGCATATATATGTGTCCAGACCCTGGCATACC	240		
Qy	241	GAAAGGGGCAAAAGCTAGGCTGGATTTCAAGTTAGATCCAGGCTCCAGTTCACTTGC	300		
Db	241	GAAAGGGGCAAAAGCTAGGCTGGATTTCAAGTTAGATCCAGGCTCCAGTTCACTTGC	300		
Qy	301	AACGAGGGCTATGACCTCGCAAGGGATCCAAAGCGGATCACTGTATGAAAGTGAAGCATG	360		
Db	301	AACGAGGGCTATGACCTCGCAAGGGATCCAAAGCGGATCACTGTATGAAAGTGAAGCATG	360		
Qy	361	TTTTCGGGCTTGAAGCGACCAAGAGCCGATGTGCAGAGCCCGCATGTGTATGCCACTT	420		
Db	361	TTTTCGGGCTTGAAGCGACCAAGAGCCGATGTGCAGAGCCCGCATGTGTATGCCACTT	420		
Qy	421	CGAGGCCCCCTCGGGCATCATCACTTCCCAATTTCCCATTCAGTATGACAAATGCA	480		
Db	421	CGAGGCCCCCTCGGGCATCATCACTTCCCAATTTCCCATTCAGTATGACAAATGCA	480		
Qy	481	CACGTGTGTGATTCATCAGCACTCAACCCCTCCAAAGGTATCAAGCTCGCTTTGAG	540		
Db	481	CACGTGTGTGATTCATCAGCACTCAACCCCTCCAAAGGTATCAAGCTCGCTTTGAG	540		
Qy	541	GAGTTTGAATTTGAGAGGGGCTATGACCCCTGACGGTCGGTGTATGTGTGATGAGTGGG	600		
Db	541	GAGTTTGAATTTGAGAGGGGCTATGACCCCTGACGGTCGGTGTATGTGTGATGAGTGGG	600		
Qy	601	GACCAAGACAGTTCTTTCATATGTCTCAAAATGCTGTGACAGACAGCCCTCAACCCCA	660		
Db	601	GACCAAGACAGTTCTTTCATATGTCTCAAAATGCTGTGACAGACAGCCCTCAACCCCA	660		
Qy	661	GGCTCTGCATCCCAAGAGCATGTCTGGGGACATCTGGAGGCAAGAAATGACTGTACTT	720		
Db	661	GGCTCTGCATCCCAAGAGCATGTCTGGGGACATCTGGAGGCAAGAAATGACTGTACTT	720		
Qy	721	GAGATCTGTGATCAATGACAGTTGACAGGTCAAGTTCAAGTGTGCA	780		

Db 721 GAGATCTGCTCGATGACATTTAGCAGTTCAATGCAAGTCAAGTTTCAGTGAAGAGCTCTCA 780  
Qy 781 AAGACTTTATATGCTGTGGAACCTTGTGCTCTGGGACAGAGATGAGCAGGGCAGTTGC 840  
Db 781 AAGACTTTATATGCTGTGGAACCTTGTGCTCTGGGACAGAGATGAGCAGGGCAGTTGC 840  
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QY 6121 CTTGCTTACCTTATGTTGGGAAATGAAATTTGACCTGCAACTTGAACTTACCTGACG 6180  
DB 6121 CTTGCTTACCTTATGTTGGGAAATGAAATTTGACCTGCAACTTGAACTTACCTGACG 6180  
QY 6181 TTTGAAGAACACCCCCGATATGTAAGTCACTGTCCAAACAAATGAGCTTCTGACAGAC 6240  
DB 6181 TTTGAAGAACACCCCCGATATGTAAGTCACTGTCCAAACAAATGAGCTTCTGACAGAC 6240  
QY 6241 TCCACAGGCGGTATCTGTAGCCAGAGCTACCTGGAAGCTATCCCAAGTTCCAGACTGC 6300  
DB 6241 TCCACAGGCGGTATCTGTAGCCAGAGCTACCTGGAAGCTATCCCAAGTTCCAGACTGC 6300  
QY 6301 TCTTGGCTGTGAGAGTGAAGCCGACCTAATACTCTCCCTCACAGTGAATCTTCTGC 6360  
DB 6301 TCTTGGCTGTGAGAGTGAAGCCGACCTAATACTCTCCCTCACAGTGAATCTTCTGC 6360  
QY 6361 AGCGAAGCAATATGATGATGATTTGATTTGATGCTTCATTCAGACAGAGTCTCTGC 6420  
DB 6361 AGCGAAGCAATATGATGATGATTTGATTTGATGCTTCATTCAGACAGAGTCTCTGC 6420  
QY 6421 CTGAAGCCCTCAGTGGGAATTAATCACTGCTCCCTGATTTGATTCAGAGCTCAAGCACTCT 6480  
DB 6421 CTGAAGCCCTCAGTGGGAATTAATCACTGCTCCCTGATTTGATTCAGAGCTCAAGCACTCT 6480  
QY 6481 GTTACCTGCTGTGATCTGATACAGCTACCGCTACATTCGGAAGGGCTTCAAGATCCGCTAT 6540  
DB 6481 GTTACCTGCTGTGATCTGATACAGCTACCGCTACATTCGGAAGGGCTTCAAGATCCGCTAT 6540  
QY 6541 TCAAGCCCTTATGACAGCTGCTCCAGAGGCTCCATTCATGCTTCAATCTAGGCCAGAC 6600  
DB 6541 TCAAGCCCTTATGACAGCTGCTCCAGAGGCTCCATTCATGCTTCAATCTAGGCCAGAC 6600  
QY 6601 AGCACCAGCCCGGGGGCTCCATTCACCTTTGCTGCAAGCGGCTACCGCTGTGGGA 6660  
DB 6601 AGCACCAGCCCGGGGGCTCCATTCACCTTTGCTGCAAGCGGCTACCGCTGTGGGA 6660  
QY 6661 CACAGCATGCGCATCTGTACCCGGGACCCCGAGGCTACCATGTGGAGCGAAGCCATC 6720  
DB 6661 CACAGCATGCGCATCTGTACCCGGGACCCCGAGGCTACCATGTGGAGCGAAGCCATC 6720  
QY 6721 CCTCTCTGCAAGCTCTTCTCTGCTGCTTCTGAGGCTCCCAAGAAATGGAATGCTT 6780  
DB 6721 CCTCTCTGCAAGCTCTTCTCTGCTGCTTCTGAGGCTCCCAAGAAATGGAATGCTT 6780  
QY 6781 GGCAGAGATACAGTGGGAACCAAGGCGTGTACAGCTGCAAGTGAAGGCTACCACTC 6840  
DB 6781 GGCAGAGATACAGTGGGAACCAAGGCGTGTGTACAGCTGCAAGTGAAGGCTACCACTC 6840  
QY 6841 CAGGACGCGCTGAGGCGCATGCAAGATGTGTGACACAGGCGTATGAGAACCGCAAT 6900  
DB 6841 CAGGACGCGCTGAGGCGCATGCAAGATGTGTGACACAGGCGTATGAGAACCGCAAT 6900  
QY 6901 GTTCCACCAAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6960  
DB 6901 GTTCCACCAAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6960  
QY 6961 GGCAGATGAGGCTTATCTTTGAGACACAGTATCAGTTCCAGGCCAGCTGATGCTATC 7020  
DB 6961 GGCAGATGAGGCTTATCTTTGAGACACAGTATCAGTTCCAGGCCAGCTGATGCTATC 7020  
QY 7021 TGTGACCTGTGCTACTATATACGTGCAAGAGGCTATCCGCTGTACAGGCCAATGGCAAA 7080

DB 7021 TGTGACCTGTGCTACTATATACGTGCAAGAGGCTATCCGCTGTACAGGCCAATGGCAAA 7080  
QY 7081 TGAAGCTCCGGGACTCTACAGCCCACTCCGGAATCAATCTCTGTGAGAGCTCCGGAAT 7140  
DB 7081 TGAAGCTCCGGGACTCTACAGCCCACTCCGGAATCAATCTCTGTGAGAGCTCCGGAAT 7140  
QY 7141 CCCCCAATGAGCCAGCATGGAACACTGTCTGTCTACAGGGGAAACAGCACTTCTCC 7200  
DB 7141 CCCCCAATGAGCCAGCATGGAACACTGTCTGTCTACAGGGGAAACAGCACTTCTCC 7200  
QY 7201 TGAATTCGGATACACTGTGTGGCTCCAGGGTGTGTGATGATGATGATGATGATGATGAT 7260  
DB 7201 TGAATTCGGATACACTGTGTGGCTCCAGGGTGTGTGATGATGATGATGATGATGATGAT 7260  
QY 7261 TGAAGTGTGTGAGT 7320  
DB 7261 TGAAGTGTGTGAGT 7320  
QY 7321 AACGACACATCAATGAGGAGAACTACAGCTACCGGGGCACTGTGTGTGTGTGTGTGTGT 7380  
DB 7321 AACGACACATCAATGAGGAGAACTACAGCTACCGGGGCACTGTGTGTGTGTGTGTGTGT 7380  
QY 7381 GCTGCTTCCGCTGTATGCGATGTCTGTGCGCATCTGTGACAGAGATCATCTGTGTG 7440  
DB 7381 GCTGCTTCCGCTGTATGCGATGTCTGTGCGCATCTGTGACAGAGATCATCTGTGTG 7440  
QY 7441 GGCAGAGCCCTTCTGT 7500  
DB 7441 GGCAGAGCCCTTCTGT 7500  
QY 7501 CTCACTCAGGGTAACTCAATGTTTAACTCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGT 7560  
DB 7501 CTCACTCAGGGTAACTCAATGTTTAACTCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGT 7560  
QY 7561 TATATGCTGAGGGGGCTGTAGGTCCCAATGCTGTGACAGGGGCAATGAGTGAATG 7620  
DB 7561 TATATGCTGAGGGGGCTGTAGGTCCCAATGCTGTGACAGGGGCAATGAGTGAATG 7620  
QY 7621 CTGCCCCACCTGACAGATCATCACTGTACAGATCTGTGACACCAAGAAATAGTGTGTGT 7680  
DB 7621 CTGCCCCACCTGACAGATCATCACTGTACAGATCTGTGACACCAAGAAATAGTGTGTGT 7680  
QY 7681 CAGTTCACAGCAGCGGCGCCAGAGGTTCACTGTGACACACTGTGTCTTACCGGATG 7740  
DB 7681 CAGTTCACAGCAGCGGCGCCAGAGGTTCACTGTGACACACTGTGTCTTACCGGATG 7740  
QY 7741 AACCAAGCTTCTTACCTCTGTGGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7800  
DB 7741 AACCAAGCTTCTTACCTCTGTGGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7800  
QY 7801 GACGCTCCCGCCAGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7860  
DB 7801 GACGCTCCCGCCAGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7860  
QY 7861 TCCAGATGTGTGAGACAGTATATCTGTGTGAGACAGTGTGTGTGTGTGTGTGTGTGTGT 7920  
DB 7861 TCCAGATGTGTGAGACAGTATATCTGTGTGAGACAGTGTGTGTGTGTGTGTGTGTGTGT 7920  
QY 7921 AAGGTATCTGT 7980  
DB 7921 AAGGTATCTGT 7980  
QY 7981 TCCCTCCCTCACTGT 8040  
DB 7981 TCCCTCCCTCACTGT 8040  
QY 8041 CATGGCATCCGTTTGGGGGACAGCTTGTATCAGGCACTGTGTGTGTGTGTGTGTGTGTGT 8100  
DB 8041 CATGGCATCCGTTTGGGGGACAGCTTGTATCAGGCACTGTGTGTGTGTGTGTGTGTGTGT 8100  
QY 8101 GCTGCGCAGTGTCTCCGGGATGCTCAGAGGCACTGTCAAGCCATGAGCTGTGTGTGTGT 8160

Db	8101	ACTGGCCACGTCGTCCTCCGGGGATTCGTCAAGGCGACCTGTCAAGCCATAGCTCTGTGGAC	8156
Qy	8161	GGCTTCGACCGTGAAGTGTGAGTATCTCTTGTGGGAAACCTTGGGACTCCAAATATGCG	8220
Db	8161	GGCTTCGACCGTGAAGTGTGAGTATCTCTTGTGGGAAACCTTGGGACTCCAAATATGCG	8220
Qy	8221	CGAGTTGTGTTCAGTGATGAGCGCTGGTTTTCTCCAGCTCTATACGTTCTATAGATGCCGGAA	8280
Db	8221	CGAGTTGTGTTCAGTGATGAGCGCTGGTTTTCTCCAGCTCTATACGTTCTATAGATGCCGGAA	8280
Qy	8281	GGATTACTACGCCACAGGCGCTGCTAGCCGCTACAGCTCCGGTCATATGGAACTGTGACAGGC	8340
Db	8281	GGATTACTACGCCACAGGCGCTGCTAGCCGCTACAGCTCCGGTCATATGGAACTGTGACAGGC	8340
Qy	8341	AGTGAACCTTGAAGTGCCTGTCATAACTGTGTGAACCTTGGGATTCAGCCAAATGACCTT	8400
Db	8341	AGTGAACCTTGAAGTGCCTGTCATAACTGTGTGAACCTTGGGATTCAGCCAAATGACCTT	8400
Qy	8401	CGGCTGGGCAATGACTTCAAGTAAACAAACAACTGTGACATATCAATGTGTCCCTGGCTAT	8460
Db	8401	CGGCTGGGCAATGACTTCAAGTAAACAAACAACTGTGACATATCAATGTGTCCCTGGCTAT	8460
Qy	8461	ATGATGAGAGTACATAGAGTATCTGTGCTGAGCTGACCAAGGACCGGACATGTGAATGGA	8520
Db	8461	ATGATGAGAGTACATAGAGTATCTGTGCTGAGCTGACCAAGGACCGGACATGTGAATGGA	8520
Qy	8521	ACCAAGCCCGCTGTGCAAGCTCTCATGTGCAAGCCACTCCGCTCATCTCCCAATGGAGAG	8580
Db	8521	ACCAAGCCCGCTGTGCAAGCTCTCATGTGCAAGCCACTCCGCTCATCTCCCAATGGAGAG	8580
Qy	8581	GTGTGGGGGTCTGACTTATGTGGGGCTCAAGTGTGACTTATGCTTGCCTGTGGAGGGTAC	8640
Db	8581	GTGTGGGGGTCTGACTTATGTGGGGGTCAAGTGTGACTTATGCTTGCCTGTGGAGGGTAC	8640
Qy	8641	CAGCTCTCCCTGCCCCGGGGGTGTCACCTGTATGGGAAATGGGCTCTGACCCGGAGACTG	8700
Db	8641	CAGCTCTCCCTGCCCCGGGGGTGTCACCTGTATGGGAAATGGGCTCTGACCCGGAGACTG	8700
Qy	8701	CCTCAGTGTGTTCCCTGTGTGTCGTGGGGGATCTGTGTGTCCTCGTCCGTTGGGAGAGAGAG	8760
Db	8701	CCTCAGTGTGTTCCCTGTGTGTCGTGGGGGATCTGTGTGTCCTCGTCCGTTGGGAGAGAGAG	8760
Qy	8761	GACCGAGGCTTCTCCTACAGGTCAATCTGTCTCTCTCTGTCACATCCCCCTCTGTGTCTG	8820
Db	8761	GACCGAGGCTTCTCCTACAGGTCAATCTGTCTCTCTCTGTCACATCCCCCTCTGTGTCTG	8820
Qy	8821	GTGGGCTTCCACGAGAGGTTTTGTCACGTCAATATGGAGCATATGGAATGGACCCACGCCAGC	8880
Db	8821	GTGGGCTTCCACGAGAGGTTTTGTCACGTCAATATGGAATGGAGCATATGGAATGGACCCACGCCAGC	8880
Qy	8881	TGCATATAGATCCGACCTGTACACGATGTGTGCGGACCTGTGTGTCACAGTTTGGGATACAG	8940
Db	8881	TGCATATAGATCCGACCTGTGTACACGATGTGTGCGGACCTGTGTGTCACAGTTTGGGATACAG	8940
Qy	8941	AACAAATTTCAAGGCTTACCAAGTGTGAAGCACAGTCTCTTTCGGTTGTCAAAAAGGCTAC	9000
Db	8941	AACAAATTTCAAGGCTTACCAAGTGTGAAGCACAGTCTCTTTCGGTTGTCAAAAAGGCTAC	9000
Qy	9001	CTGCTTTCAGGGCTCCACACCAAGGACCTGCTCTCCCAACCTGACCTTGAATGGAACCCCA	9060
Db	9001	CTGCTTTCAGGGCTCCACACCAAGGACCTGCTCTCCCAACCTGACCTTGAATGGAACCCCA	9060
Qy	9061	CCTGACTGTATCCCCACCACTGACAGGACGACAGACGCCAAGCATGCCACGTGGGG	9120
Db	9061	CCTGACTGTATCCCCACCACTGACAGGACGACAGACGCCAAGCATGCCACGTGGGG	9120
Qy	9121	GCCCTGATTTTGCCTCTCATAGGCTACACGCTCATTAATCTCTGTCAGAGAGGCTTCTCC	9180
Db	9121	GCCCTGATTTTGCCTCTCATAGGCTACACGCTCATTAATCTCTGTCAGAGAGGCTTCTCTCC	9180
Qy	9181	TCAAGGGTGTGCTCCGAGACCGGACCTTGCAAGGGGATGCGAGCTGGACAGGACGCGC	9240
Db	9181	TCAAGGGTGTGCTCCGAGACCGGACCTTGCAAGGGGATGCGAGCTGGACAGGACGCGC	9240

QY	9241	CCATCTCCCTGAGAGAGTCCGGCCCAAGTGGAGACCCATCAACAATGCGCCGGAGCCACCGC	9300
Db	9241	CCATCTCCCTGAGAGTCCGGCCCAAGTGGAGACCCATCAACAATGCGCCGGAGCCACCGC	9300
QY	9301	TCACCCCAAGCCTTGATTCCTGCGGGAATGTTTTTTCCAAGAAATTCCTCGTGGAAAGGGGCTT	9360
Db	9301	TCACCCCAAGCCTTGATTCCTGCGGGAATGTTTTTTCCAAGAAATTCCTCGTGGAAAGGGGCTT	9360
QY	9361	ATGAATACCAAGGGAGAAAGACAGCAGCCATGCTCAAGTGACTGGCTTCCAAATTGGCCA	9420
Db	9361	ATGAATACCAAGGGAGAAAGACAGCAGCCATGCTCAAGTGACTGGCTTCCAAATTGGCCA	9420
QY	9421	ACACCAAGATCAATAGCCACATGATGGAACCAAGTGGCGGTGGAGCTGCACTTGGCTGGAA	9480
Db	9421	ACACCAAGATCAATAGCCACATGATGGAACCAAGTGGCGGTGGAGCTGCACTTGGCTGGAA	9480
QY	9481	CTTACAAGAAAGAAATTTTCATCTCCTCACTCCAGGTGTACACAGATTAACAGGGCCCTGTGG	9540
Db	9481	CTTACAAGAAAGAAATTTTCATCTCCTCACTCCAGGTGTACACAGATTAACAGGGCCCTGTGG	9540
QY	9541	AGATCTTTAATGAATAAGTTCAAAAGATGATCACTGGGCTTTAATGGCCAATGCTCGTCAAG	9600
Db	9541	AGATCTTTAATGAATAAGTTCAAAAGATGATCACTGGGCTTTAATGGCCAATGCTCGTCAAG	9600
QY	9601	AGTCTCCGGAGCCACCTTCATCTACCAAGGCTCTGTCAAGGGGCCAAGGCTTTGGGCACT	9660
Db	9601	AGTCTCCGGAGCCACCTTCATCTACCAAGGCTCTGTCAAGGGGCCAAGGCTTTGGGCACT	9660
QY	9661	TCGGCTTTCAAGAAGCTGGAAGCTGAGGCTGTGTGAGTCAAGACCCCGAGTCCATTGGCGCGC	9720
Db	9661	TCGGCTTTCAAGAAGCTGGAAGCTGAGGCTGTGTGAGTCAAGACCCCGAGTCCATTGGCGCGC	9720
QY	9721	ACTTTGCTTCCAAGAGAGCTCAAGTGGCAGCCCGCATCTGTGTGCTTTCAATCGCCTCA	9780
Db	9721	ACTTTGCTTCCAAGAGAGCTCAAGTGGCAGCCCGCATCTGTGTGCTTTCAATCGCCTCA	9780
QY	9781	TTATTGGGGGGTTGATCTCTAATCTCTACAAGACAGAGAAAGACCCAAAGTTCCCTTTCA	9840
Db	9781	TTATTGGGGGGTTGATCTCTAATCTCTACAAGACAGAGAAAGACCCAAAGTTCCCTTTCA	9840
QY	9841	ATGGCTATGTGCGCCAGAGAACCAATGTTGGGCCCACTTTTGAAGACCCAATGTAGC	9900
Db	9841	ATGGCTATGTGCGCCAGAGAACCAATGTTGGGCCCACTTTTGAAGACCCAATGTAGC	9900
QY	9901	ACCGCAATTCAGACCCCAAGACATCATGATGACGACGAGGCGGATTCACAGTCAGACACAG	9960
Db	9901	ACCGCAATTCAGACCCCAAGACATCATGATGACGACGAGGCGGATTCACAGTCAGACACAG	9960
QY	9961	TGTGCACAGCAGTATGATGCAACCCGGGCTGGCCGCTTTTTTGTGATGAGTGAAGTGGTACT	10020
Db	9961	TGTGCACAGCAGTATGATGCAACCCGGGCTGGCCGCTTTTTTGTGATGAGTGAAGTGGTACT	10020
QY	10021	CCAGCAGCCGCGCGAAGCTGTGACTGTGCTGCATCTCAAGCTCACTGCAACCTCCCTGC	10080
Db	10021	CCAGCAGCCGCGCGAAGCTGTGACTGTGCTGCATCTCAAGCTCACTGCAACCTCCCTGC	10080
QY	10081	CTGATTTCCCTGCTCAGCTGCGCGAGTGGCTGCTCCGATTCGAGGCGCGCACCCGCCAC	10136
Db	10081	CTGATTTCCCTGCTCAGCTGCGCGAGTGGCTGCTCCGATTCGAGGCGCGCACCCGCCAC	10136

KW anorectic; antidiabetic; antimicrobial; antipneumonic; gene therapy;  
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
 KW obesity; diabetes; infectious disease; metabolic syndrome X;  
 KW dyslipidaemia.  
 OS Homo sapiens.  
 PN WO2003102155-A2.  
 XX 11-DEC-2003.  
 XX 03-JUN-2003; 2003WO-US017430.  
 PF 03-JUN-2003; 2002US-0385120P.  
 PR 03-JUN-2003; 2002US-0385120P.  
 PR 04-JUN-2003; 2002US-0385784P.  
 PR 05-JUN-2003; 2002US-0386041P.  
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 PR 06-JUN-2003; 2002US-0386376P.  
 PR 06-JUN-2003; 2002US-0386453P.  
 PR 06-JUN-2003; 2002US-0386864P.  
 PR 06-JUN-2003; 2002US-0387016P.  
 PR 07-JUN-2003; 2002US-0387966P.  
 PR 07-JUN-2003; 2002US-0388161P.  
 PR 07-JUN-2003; 2002US-0388311P.  
 PR 07-JUN-2003; 2002US-03885942P.  
 PR 07-JUN-2003; 2002US-03886971P.  
 PR 07-JUN-2003; 2002US-0387262P.  
 PR 08-JUN-2003; 2002US-0296960P.  
 PR 10-JUN-2003; 2002US-0387400P.  
 PR 10-JUN-2003; 2002US-0387535P.  
 PR 11-JUN-2003; 2002US-0387610P.  
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 PR 12-JUN-2003; 2002US-0387934P.  
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 PR 14-JUN-2003; 2002US-0389118P.  
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 PR 14-JUN-2003; 2002US-0389146P.  
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 PR 18-JUN-2003; 2002US-0389884P.  
 PR 19-JUN-2003; 2002US-0390066P.  
 PR 19-JUN-2003; 2002US-0390763P.  
 PR 21-JUN-2003; 2002US-0390763P.  
 PR 17-JUL-2003; 2002US-0396706P.  
 PR 06-AUG-2003; 2002US-0401628P.  
 PR 09-AUG-2003; 2002US-0402156P.  
 PR 09-AUG-2003; 2002US-0402256P.  
 PR 09-AUG-2003; 2002US-0402389P.  
 PR 12-AUG-2003; 2002US-0402786P.  
 PR 12-AUG-2003; 2002US-0402816P.  
 PR 12-AUG-2003; 2002US-0402821P.  
 PR 12-AUG-2003; 2002US-0402832P.  
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 PR 13-AUG-2003; 2002US-0403459P.  
 PR 13-AUG-2003; 2002US-0403531P.  
 PR 13-AUG-2003; 2002US-0403532P.  
 PR 13-AUG-2003; 2002US-0403563P.  
 PR 13-AUG-2003; 2002US-0406317P.  
 PR 15-AUG-2003; 2002US-0406177P.  
 PR 26-AUG-2003; 2002US-0406182P.  
 PR 26-AUG-2003; 2002US-0406355P.  
 PR 27-AUG-2003; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.  
 PR 20-SEP-2002; 2002US-0412528P.  
 PR 23-SEP-2002; 2002US-0412731P.  
 PR 30-SEP-2002; 2002US-0414801P.  
 PR 30-SEP-2002; 2002US-0414839P.  
 PR 30-SEP-2002; 2002US-0414840P.  
 PR 30-SEP-2002; 2002US-0414954P.  
 PR 09-OCT-2002; 2002US-0417186P.  
 PR 09-OCT-2002; 2002US-0417406P.  
 PR 23-OCT-2002; 2002US-0420639P.  
 PR 28-OCT-2002; 2002US-0421156P.  
 PR 31-OCT-2002; 2002US-0422690P.  
 PR 01-NOV-2002; 2002US-0423130P.  
 PR 05-NOV-2002; 2002US-0423798P.  
 PR 05-NOV-2002; 2002US-0423798P.  
 PR 12-NOV-2002; 2002US-0425453P.  
 XX  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Alebrock JP, Alvarez E, Anderson DW, Boldog FL, Caeman SJ;  
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
 PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;  
 PI Guev VY, Hermann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
 PI MacLachlan T, Malyankar UM, Mezick AJ, Miller I, Mishra VS, Raetelli L;  
 PI Padigaru M, Patturajan M, Pena GA, Peyman JA, Raha D, Raetelli L;  
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;  
 PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;  
 PI Zhong H;  
 XX  
 DR WPI; 2004-081935/08.  
 DR P-PSDB; ADH71142.  
 XX  
 PT New NOXV polypeptides and nucleic acid molecules useful for preventing or  
 PT treating NOXV-associated disorders, e.g. cancer, diabetes, infection or  
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
 XX  
 PS Example 4; SEQ ID NO 37; 1880pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide (NOXV). A  
 CC polypeptide of the invention has cytostatic, immunomodulator,  
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
 CC antipneumonic activity, and may have a use in gene therapy, and as a  
 CC vaccine. The polypeptides are encoded by NOXV polynucleotides comprising  
 CC any of the 303 fully defined nucleotide sequences given in the  
 CC specification. The polypeptide is useful in the manufacture of a  
 CC medicament for treating a syndrome associated with a human disease. The  
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
 CC treating or preventing NOXV-associated disorders, e.g. cancer, cachexia,  
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
 CC further used as hybridisation probes, in chromosome mapping, tissue  
 CC typing, preventive medicine, and pharmacogenomics. The present sequence  
 CC encodes a NOXV polypeptide of the invention.  
 XX  
 SQ Sequence 9951 BP; 2118 A; 2982 C; 2697 G; 2154 T; 0 U; 0 Other;  
 Query Match 95.8%; Score 9710.4; DB 12; Length 9951;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 9942; Conservative 0; Mismatches 1; Indels 201; Gaps 3;  
 QY 1 ATGGGGGGGCGCCCTCCCGCGCTTGTGCTGCTGCTGCACTTGTGATTCGACGCTGCT 60  
 DB 1 ATGGGGGGGCGCCCTCCCGCGCTTGTGCTGCTGCTGCACTTGTGATTCGACGCTGCT 60  
 QY 61 GCTAGCATTCAGGACATTCCTGGGCGCTAGACCTCCGAGCTAGTGAAGAGCAATT 120  
 DB 61 GCTAGCATTCAGGACATTCCTGGGCGCTAGACCTCCGAGCTAGTGAAGAGCAATT 120  
 QY 121 GAGTGAAGTCTCGAGGTGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 DB 121 GAGTGAAGTCTCGAGGTGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 QY 181 GTGTTACTCAGGTGTGTGTGTGTCGACAGACATATATGTGTGCTGACACCTGGCATACC 240



Db	181	GTGTTAACTCAGGTTGGTGTGTGTCCCAAGACATTAATATGTGTCCAGACCTTGGCATACC	240
Qy	241	GAAGAGGGCAAAAGCTAGAGCTCGGATTTCAAGTTAGGATCCAGGCTCAGTTCACTTC	300
Db	241	GAAGAGGGCAAAAGCTAGAGCTCGGATTTCAAGTTAGGATCCAGGCTCAGTTCACTTC	300
Qy	301	AACGAGGGCTATGACCTTCGCAAGGGTTCGAAGGGGATCACTCTGTATGAAGTGAAGCATG	360
Db	301	AACGAGGGCTATGACCTTCGCAAGGGTTCGAAGGGGATCACTCTGTATGAAGTGAAGCATG	360
Qy	361	TTTGGGGCTGGAAGGACCAACAGGCTGTGGAGCCGAGCCGATGTGATGCCACCTT	420
Db	361	TTTGGGGCTGGAAGGACCAACAGGCTGTGGAGCCGAGCCGATGTGATGCCACCTT	420
Qy	421	CGAGGCCCTCGGGCATCATCACTCCCAATTTCCCATTCAGTATGACAAACATGCA	480
Db	421	CGAGGCCCTCGGGCATCATCACTCCCAATTTCCCATTCAGTATGACAAACATGCA	480
Qy	481	CACGTGTGTGGATATCATCAGCACTCAACCCCTCCAGAGTATCAACCTCGCTTTGAG	540
Db	481	CACGTGTGTGGATATCATCAGCACTCAACCCCTCCAGAGTATCAACCTCGCTTTGAG	540
Qy	541	GAGTTGATTTGGAGAGGGGCTATGACACCCCTGAACGTCGGTATGTGTGTACGATGGG	600
Db	541	GAGTTGATTTGGAGAGGGGCTATGACACCCCTGAACGTCGGTATGTGTGTACGATGGG	600
Qy	601	GACCAAGAACAGTTCTCTACATGTCTCAAAAATGCTCAGTGAACGCTTCACACCCA	660
Db	601	GACCAAGAACAGTTCTCTACATGTCTCAAAAATGCTCAGTGAACGCTTCACACCCA	660
Qy	661	GGCTCTCGCATCCAGAGACATGTCTGGGGAATCTGAGGCAAGAAATGACCTGTACTT	720
Db	661	GGCTCTCGCATCCAGAGACATGTCTGGGGAATCTGAGGCAAGAAATGACCTGTACTT	720
Qy	721	GAGATCTGTCCGTAATTAGCATTTCAATGCAAGTCAAGTCAAGTTCAGTAGAAGTCTCA	780
Db	721	GAGATCTGTCCGTAATTAGCATTTCAATGCAAGTCAAGTTCAGTAGAAGTCTCA	780
Qy	781	AAGAATTCTAATGCTGTGAAACTTTGTTCTCTCCGTGGAACAGAGATGACAGGGCAGTTGC	840
Db	781	AAGAATTCTAATGCTGTGAAACTTTGTTCTCTCCGTGGAACAGAGATGACAGGGCAGTTGC	840
Qy	841	GGTGAACCTTGATACCTGCAATATGAGCCGAGAGGAAGGCTCCCGGTTTCACACGGTAGC	900
Db	841	GGTGAACCTTGATACCTGCAATATGAGCCGAGAGGAAGGCTCCCGGTTTCACACGGTAGC	900
Qy	901	ACACTCAAGTTTGAATGCGCAGCCGCTTTGAGCTGTGTGTGGACAGAAAGGCAATCAATGC	960
Db	901	ACACTCAAGTTTGAATGCGCAGCCGCTTTGAGCTGTGTGTGGACAGAAAGGCAATCAATGC	960
Qy	961	CAAAAGATTAACCAATGGTCGGCTTAAGAAAGCAGGCTGAGTTCCTCGGCTTTTCAAC	1020
Db	961	CAAAAGATTAACCAATGGTCGGCTTAAGAAAGCAGGCTGAGTTCCTCGGCTTTTCAAC	1020
Qy	1021	TTCAACAGCCGCTCTGGGTTGTCTCTGTCTCCCACTACCAAGAGACTATAGGCACACAC	1080
Db	1021	TTCAACAGCCGCTCTGGGTTGTCTCTGTCTCCCACTACCAAGAGACTATAGGCACACAC	1080
Qy	1081	CTCCACTGTGTCTGCTCATCTCTGGCCAGGCTGTGAAGCCGATCACTGGCTTTCAAC	1140
Db	1081	CTCCACTGTGTCTGCTCATCTCTGGCCAGGCTGTGAAGCCGATCACTGGCTTTCAAC	1140
Qy	1141	GACATTTGACGTGAGACCTTCAAGTTTAATTTCCGTGCATCAAGAGATGGGGCCACCGCCGAG	1200
Db	1141	GACATTTGACGTGAGACCTTCAAGTTTAATTTCCGTGCATCAAGAGATGGGGCCACCGCCGAG	1200
Qy	1201	GGCCCGCTCTGGGCACTTCTCAGAAACCAAGTTCCTCTCCATCAACAAGCATGTGC	1260
Db	1201	GGCCCGCTCTGGGCACTTCTCAGAAACCAAGTTCCTCTCCATCAACAAGCATGTGC	1260
Qy	1261	CACGTGGCCGCTCTGAGTTCCAGACTGACCTTCACAGGAGAGGGGCTTCAACATC	1320

Db	1261	AACGTGGCCCGCTCGAGTTCCAGACTGACACTCCACAGGGAAGAGGGGCTTCAACATC	1320
Qy	1321	ACCTTTACCACTTCCGACACACAGAGTCCCGGATCTTGCGCTTCCAGTAAATGGCAMA	1380
Db	1321	ACTTTTACCACTTCCGACACAAAGAGGCCCGGATCTTGCGCTTCCAGTAAATGGCAMA	1380
Qy	1381	CGGTTTGGGGGACACCTCCAGCTGGGGAGGCTCCATCTCCCTTCCCTGTGATGAAGGCTTC	1440
Db	1381	CGGTTTGGGGGACACCTCCAGCTGGGGAGGCTCCATCTCTCTCTGTGATGAAGGCTTC	1440
Qy	1441	CTTGGGACCTAGGGGCTCAGAGACCATCAGCTGCCTCGTGAAGAGGGGACGGTGTCTGG	1500
Db	1441	CTTGGGACCTAGGGGCTCAGAGACCATCAGCTGCCTCGTGAAGAGGGGACGGTGTCTGG	1500
Qy	1501	AACAGCGCTGTGCTCGGCTGTGANGCTCCTGTGTGTACTCTGACTTGGCCAGCGGC	1560
Db	1501	AACAGCGCTGTGCTCGGCTGTGANGCTCCTGTGTGTGTACTCTGACTTGGCCAGCGGC	1560
Qy	1561	ACCATCTCTCTCCGGGCTGGCGCTGGCTTCTACAAAGATGCTTGACTGTGCTGGGTTG	1620
Db	1561	ACCATCTCTCTCCGGGCTGGCGCTGGCTTCTACAAAGATGCTTGACTGTGCTGGGTTG	1620
Qy	1621	ATTGAGGCGCCAGGAGGCTACCCCATCAAAATCACTTCCAGACATTCMAAACCGAGGTC	1680
Db	1621	ATTGAGGCGCCAGGAGGCTACCCCATCAAAATCACTTCCAGACATTCMAAACCGAGGTC	1680
Qy	1681	AACATAAGCACCCCTGGAGATACGGGATGGGCGGACTTACTCAGGCGCTTGATCGGGGTT	1740
Db	1681	AACATAAGCACCCCTGGAGATACGGGATGGGCGGACTTACTCAGGCGCTTGATCGGGGTT	1740
Qy	1741	TACCAAGGGAGACCCAGGTTCCCAATCTCTCATAGCACACAGCACTACCTCTACTCTCTC	1800
Db	1741	TACCAAGGGAGACCCAGGTTCCCAATCTCTCATAGCACACAGCACTACCTCTACTCTCTC	1800
Qy	1801	TTCTCTACCGACAAGAGTCACTCGGACATCGGCTTCCAGCTCCGCTAATGAGACTATAACA	1860
Db	1801	TTCTCTACCGACAAGAGTCACTCGGACATCGGCTTCCAGCTCCGCTAATGAGACTATAACA	1860
Qy	1861	CTGCAGTCAGACCACTGTCTGGATCCAGGAATCCCAAGTAAATGAGACAGCGTCATGGGAT	1920
Db	1861	CTGCAGTCAGACCACTGTCTGGATCCAGGAATCCCAAGTAAATGAGACAGCGTCATGGGAT	1920
Qy	1921	GACTTCTACGCTGGGCGCGCTGTGATCCTTCAAGCTGTGACTCTGGGCTACACTTAAATGAC	1980
Db	1921	GACTTCTACGCTGGGCGCGCTGTGATCCTTCAAGCTGTGACTCTGGGCTACACTTAAATGAC	1980
Qy	1981	GGGGAGCGCTCGAGGTGTGAGCCCACTTCCAGTGTGAGCGGGGCGTGGCCAGTTGTGAA	2040
Db	1981	GGGGAGCGCTCGAGGTGTGAGCCCACTTCCAGTGTGAGCGGGGCGTGGCCAGTTGTGAA	2040
Qy	2041	GCTCTGTGTGTGGCTTCAATCAAGAGCTCCAGTGGGACCACTTGTGTGCGCAGGGTCCCT	2100
Db	2041	GCTCTGTGTGTGGCTTCAATCAAGAGCTCCAGTGGGACCACTTGTGTGCGCAGGGTCCCT	2100
Qy	2101	GACTTCTACCCCAACACTTGAACCTGCACTGTATTCGAAACATCTCATGTGCGCAAGGCT	2160
Db	2101	GACTTCTACCCCAACACTTGAACCTGCACTGTATTCGAAACATCTCATGTGCGCAAGGCT	2160
Qy	2161	GTTGTTTTCATTTTCCACACTTCCACTGTGAAAGTGGCAATGACTCTCTCTCATCACT	2220
Db	2161	GTTGTTTTCATTTTCCACACTTCCACTGTGAAAGTGGCAATGACTCTCTCTCATCACT	2220
Qy	2221	GAGAAAGGACACTTCAACCCAGCGCTGTGAGGAGCTAACTGGATCTCGGCTGCGCAGCTCC	2280
Db	2221	GAGAAAGGACACTTCAACCCAGCGCTGTGAGGAGCTAACTGGATCTCGGCTGCGCAGCTCC	2280
Qy	2281	ATCAGCGCTGGGCTCTATGAGCACTTCACTGACCTCCAGGATCGGCTTCACTCTGATTTCTCC	2340
Db	2281	ATCAGCGCTGGGCTCTATGAGCACTTCACTGACCTCCAGGATCGGCTTCACTCTGATTTCTCC	2340
Qy	2341	ATGTCATATGAAGATTCACATCACTTCCAGATGACACTTGGAGCGCTGTGAGAGG	2400
Db	2341	ATGTCATATGAAGATTCACATCACTTCCAGATGACACTTGTGAGAGCGCTGTGAGAGG	2400



QY 2401 CCCGAGTCCCACTACAGCATCCGAAAGGCTTGACATTGGCGTGGCGACACCTTG 2460  
DB 2401 CCCGAGTCCCACTACAGCATCCGAAAGGCTTGACATTGGCGTGGCGACACCTTG 2460  
QY 2461 ACCCTTCTCTGCTTCCCGGGGTACCGTCTGAGAGGACCCGCCATACGTGCTGGG 2520  
DB 2461 ACCCTTCTCTGCTTCCCGGGGTACCGTCTGAGAGGACCCGCCATACGTGCTGGG 2520  
QY 2521 GCGCAACGCGCGCTGAGAGCTGCGCTGCAAGTGTGTGAGTGTGGGAATTCA 2580  
DB 2521 GCGCAACGCGCGCTGAGAGCTGCGCTGCAAGTGTGTGAGTGTGGGAATTCA 2580  
QY 2581 GTACAGAGCACTCAGGGTACTTGTGCTGCTCCCACTTCTGTGAACTACATPAACAT 2640  
DB 2581 GTACAGAGCACTCAGGGTACTTGTGCTGCTCCCACTTCTGTGAACTACATPAACAT 2640  
QY 2641 CATGAATGATCTACTCCATCCAGACCCAGCCAGGGAAATTCAGCTGAAAGCCAG 2700  
DB 2641 CATGAATGATCTACTCCATCCAGACCCAGCCAGGGAAATTCAGCTGAAAGCCAG 2700  
QY 2701 GCATTGCACTCTCCGAGAGAGTGTCTCAAGTTTATGATGCAACAACAATCCGCC 2760  
DB 2701 GCATTGCACTCTCCGAGAGAGTGTCTCAAGTTTATGATGCAACAACAATCCGCC 2760  
QY 2761 CGTTTGTGAGAGTTTATGACCATTTCTGATGATGAGGGGTGACTTTGAAACGACATCC 2820  
DB 2761 CGTTTGTGAGAGTTTATGACCATTTCTGATGATGAGGGGTGACTTTGAAACGACATCC 2820  
QY 2821 AGCAGTGTGTGCTTATTCATCACTGATGCTGAAACACAGCAGAGGGCTTTGAACTG 2880  
DB 2821 AGCAGTGTGTGCTTATTCATCACTGATGCTGAAACACAGCAGAGGGCTTTGAACTG 2880  
QY 2881 CACTTTCCAGCTTTGAACTCAATCAATGTAGAGACCCAGAACCCCAAGTTTGCTAC 2940  
DB 2881 CACTTTCCAGCTTTGAACTCAATCAATGTAGAGACCCAGAACCCCAAGTTTGCTAC 2940  
QY 2941 AAGGTTATGATGATGATCAATTTTGGAGAGAGTCCGTGCTTCAAGCTGATACCTGGA 3000  
DB 2941 AAGGTTATGATGATGATCAATTTTGGAGAGAGTCCGTGCTTCAAGCTGATACCTGGA 3000  
QY 3001 TACAGCTGCGGGGTAGTAGAGAGTGTCTGATGAGAGCGCCGACCTTGGAAC 3060  
DB 3001 TACAGCTGCGGGGTAGTAGAGAGTGTCTGATGAGAGCGCCGACCTTGGAAC 3060  
QY 3061 CGGCTCTGCGCACTGTGTGCGCGAGTGTGAGAGGACAGTGAAGAGAGGTGCGGG 3120  
DB 3061 CGGCTCTGCGCACTGTGTGCGCGAGTGTGAGAGGACAGTGAAGAGAGGTGCGGG 3120  
QY 3121 CAGGTGTGTCACTCCCGGGTATCCAGCTCCCTATGAAACAATCTCAACTGATCTGAGC 3180  
DB 3121 CAGGTGTGTCACTCCCGGGTATCCAGCTCCCTATGAAACAATCTCAACTGATCTGAGC 3180  
QY 3181 ATCGAAGCAGAGCGCGCTGCAACCATTTGACTTCTGTGTGTTGACAGAGAGAG 3240  
DB 3181 ATCGAAGCAGAGCGCGCTGCAACCATTTGACTTCTGTGTGTTGACAGAGAGAG 3240  
QY 3241 GTTACGACGTGTGCGCATCTGAGATGAGGCTGTGAGAGCGGGGTGTGCTGAAGAG 3300  
DB 3241 GTTACGACGTGTGCGCATCTGAGATGAGGCTGTGAGAGCGGGGTGTGCTGAAGAG 3300  
QY 3301 CTGAGTGGCGCGCGCTGCGCAAGACCTGATAGCACTTCAACTGATGCTGCTGAG 3360  
DB 3301 CTGAGTGGCGCGCGCTGCGCAAGACCTGATAGCACTTCAACTGATGCTGCTGAG 3360  
QY 3361 TTGACACTGACTTCTTCAACGAGACAGAGGCTTTGCCATTTCAATTTTCAAGTGTCA 3420  
DB 3361 TTGACACTGACTTCTTCAACGAGACAGAGGCTTTGCCATTTCAATTTTCAAGTGTCA 3420  
QY 3421 GCAACGTCTTCAATGACCTTGGAGTCCCGAGATGAGAGTGGAGTGGAGTGGACAGTTGG 3480  
DB 3421 GCAACGTCTTCAATGACCTTGGAGTCCCGAGATGAGAGTGGAGTGGAGTGGACAGTTGG 3480

QY 3481 GAAGCGGAGACTCCACAGTGTTCAGATGTGACCCCTGCTACGCGCTGAGAGGAGTGCA 3540  
DB 3481 GAAGCGGAGACTCCACAGTGTTCAGATGTGACCCCTGCTACGCGCTGAGAGGAGTGCA 3540  
QY 3541 GAGATCAGCTGTGTGAAATGACAGAAACAGGTTCTTTGCGACGCCAGCCGCCAATGTC 3600  
DB 3541 GAGATCAGCTGTGTGAAATGACAGAAACAGGTTCTTTGCGACGCCAGCCGCCAATGTC 3600  
QY 3601 ATGCTTCTGCGGGGAGAACTGACAGAACATCTGAGGTATCTCTCACCAATTAC 3660  
DB 3601 ATGCTTCTGCGGGGAGAACTGACAGAACATCTGAGGTATCTCTCACCAATTAC 3660  
QY 3661 CCAGAACCCATCCCGCAGAGCAAGAGTGTGACTGGAAGTGAACCGTCTCACAGACTAC 3720  
DB 3661 CCAGAACCCATCCCGCAGAGCAAGAGTGTGACTGGAAGTGAACCGTCTCACAGACTAC 3720  
QY 3721 GTCATGCGCTGTGATTTAACTTTTAACTTGAACCTGAGACCTGCTATGACTTCTCCATAC 3780  
DB 3721 GTCATGCGCTGTGATTTAACTTTTAACTTGAACCTGAGACCTGCTATGACTTCTCCATAC 3780  
QY 3781 TACGAGAGAGGAGCTCTGACGCGCTCTCATGGAAGCTTCTATGCTCCAGCTCCCA 3840  
DB 3781 TACGAGAGAGGAGCTCTGACGCGCTCTCATGGAAGCTTCTATGCTCCAGCTCCCA 3840  
QY 3841 GCGCGATTGAAAGCAGACAGCAACAGCTTCTGCTGCGCTTCCGACGATCATCTGTG 3900  
DB 3841 GCGCGATTGAAAGCAGACAGCAACAGCTTCTGCTGCGCTTCCGACGATCATCTGTG 3900  
QY 3901 AGCAGTGTGCTTCTGCTCATTTGACTATACAGAAACCCCGGGAGTATGTTGATCTT 3960  
DB 3901 AGCAGTGTGCTTCTGCTCATTTGACTATACAGAAACCCCGGGAGTATGTTGATCTT 3960  
QY 3961 GGTTCATCAAGAACGAGCACAGGAGTGGGTCCGACTGGAAGCTTCTGCTGAC 4020  
DB 3961 GGTTCATCAAGAACGAGCACAGGAGTGGGTCCGACTGGAAGCTTCTGCTGAC 4020  
QY 4021 TACTACTGCAAGGAGGCTTCAAGATTGAGAGGACCTTCAACCTGAGTGTGATCTGAGG 4080  
DB 4021 TACTACTGCAAGGAGGCTTCAAGATTGAGAGGACCTTCAACCTGAGTGTGATCTGAGG 4080  
QY 4081 CCTATGAGAAAGCCCGTGTGAAACAATCCCGGCACTGACAGAGCCCTGAGGAGG 4140  
DB 4081 CCTATGAGAAAGCCCGTGTGAAACAATCCCGGCACTGACAGAGCCCTGAGGAGG 4140  
QY 4141 CAGTATGAGGTTGAGACGAGAGTGTGCTTGTCCCACTACCCCGAAGTACACCACT 4200  
DB 4141 CAGTATGAGGTTGAGACGAGAGTGTGCTTGTCCCACTACCCCGAAGTACACCACT 4200  
QY 4201 GAGCAGATCTGCTGATTTTGTACTGTGCCCCAAGACATATGTGTGTGCTTGGCAGTTC 4260  
DB 4201 GAGCAGATCTGCTGATTTTGTACTGTGCCCCAAGACATATGTGTGTGCTTGGCAGTTC 4260  
QY 4261 GCGTTCTTTCACAGGCGCTTCAACGAGTGTGAGGTTACAGAGGCGCACAGCAGAGC 4320  
DB 4261 GCGTTCTTTCACAGGCGCTTCAACGAGTGTGAGGTTACAGAGGCGCACAGCAGAGC 4320  
QY 4321 TCGCGGCTCTCAAGTCTTCTGAGGCTCCCATACAGAGATCACTGCTTGGCCACC 4380  
DB 4321 TCGCGGCTCTCAAGTCTTCTGAGGCTCCCATACAGAGATCACTGCTTGGCCACC 4380  
QY 4381 TCCATCAAGTTCTATTAATTTAGAGGCGCAAGAGGCTTCCAGCAGCAGAGGCTTCCAC 4440  
DB 4381 TCCATCAAGTTCTATTAATTTAGAGGCGCAAGAGGCTTCCAGCAGCAGAGGCTTCCAC 4440  
QY 4441 TTTGTCTACAGAGGCTTCTGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCC 4500  
DB 4441 TTTGTCTACAGAGGCTTCTGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCC 4500  
QY 4501 GCGTATGAGAGGCTTGGGAGTGTGACTTCTGCGTGGGGGCAATGCTGCTGCAATGTC 4560  
DB 4501 GCGTATGAGAGGCTTGGGAGTGTGACTTCTGCGTGGGGGCAATGCTGCTGCAATGTC 4560  
QY 4561 AACTCCGCTAGCCCTGACAGGAGTCCGACAGATGAGTGTGCTGCTGCTGCTGCTGCTGCT 4620  
DB 4561 AACTCCGCTAGCCCTGACAGGAGTCCGACAGATGAGTGTGCTGCTGCTGCTGCTGCTGCT 4620

Db	4561	AACTCCGGCTATGCCCTCGAAGGAGTCCGCAAGATCGATGCTCCCTGTGCTCGGGCC	4620
Qy	4621	TTGGCCCAATGGAATGATCTCAGCGCCACGATGTGTGGCCGTGGAGCACTCA	4680
Db	4621	TTGGCCCAATGGAATGTCTCAGCGCCACGATGTGTGGCCGTGGAGCACTCA	4680
Qy	4661	GAGCCGAGGGGCAACATCTCTGTCCCTTGGCTTCCAGACCGTACCTCAACGCTCAAC	4740
Db	4661	GAGCCGAGGGGCAACATCTCTGTCCCTTGGCTTCCAGACCGTACCTCAACGCTCAAC	4740
Qy	4741	TGTGTGTGAAGATGTGTGTGCCCGAAGGCGGTGGACCTCCAGATCCAAAGTTGACATTTT	4800
Db	4741	TGTGTGTGAAGATGTGTGTGCCCGAAGGCGGTGGACCTCCAGATCCAAAGTTGACATTTT	4800
Qy	4801	GTGACAGAGCAGAACTGGGACTCGCTGGAAAGTATTGATGGTCAGATTAACCTGTAAAC	4860
Db	4801	GTGACAGAGCAGAACTGGGACTCGCTGGAAAGTATTGATGGTCAGATTAACCTGTAAAC	4860
Qy	4861	ATGCTGGGAGATTCTTCAGAAACAACGCTGCTGCTTCTGAAACAGCACTTCAACCAAG	4920
Db	4861	ATGCTGGGAGATTCTTCAGAAACAACGCTGCTGCTTCTGAAACAGCACTTCAACCAAG	4920
Qy	4921	CTCTAACCTTCATTCTTACTCAGATTAACAAGCGATCTGACAGCTGGCTTCACTTGAATAC	4980
Db	4921	CTCTAACCTTCATTCTTACTCAGATTAACAAGCGATCTGACAGCTGGCTTCACTTGAATAC	4980
Qy	4981	AAAACGGTGGGCTCAGCAGTTGTCCGGAACCTGTGTGCCAGATTAACGGGGTGAAGCT	5040
Db	4981	AAAACGGTGGGCTCAGCAGTTGTGTCCGGAACCTGTGTGCCAGATTAACGGGGTGAAGCT	5040
Qy	5041	GCGCAGCGCTACTTGTGTGAATGATGTGTGTTCTTTCAGATGTGACCGGGAATATGCCCTC	5100
Db	5041	GCGCAGCGCTACTTGTGTGAATGATGTGTGTTCTTTCAGATGTGACCGGGAATATGCCCTC	5100
Qy	5101	CAGGGCCACGCCCAATCTCTCTGCATGCCCCGGAACAGTGGCGCAATGAACTTACCCTCT	5160
Db	5101	CAGGGCCACGCCCAATCTCTCTGCATGCCCCGGAACAGTGGCGCAATGAACTTACCCTCT	5160
Qy	5161	CCACTCTGTATTGTCACAGTGTGGGGGAACAGTGGAGAGATGGAAGGGGTATCTGTAGC	5220
Db	5161	CCACTCTGTATTGTCACAGTGTGGGGGAACAGTGGAGAGATGGAAGGGGTATCTGTAGC	5220
Qy	5221	CCCGGCTTCCAGGCACTACCCCAAGTAACATGACTCTCTCTGAAAATATGACTGTGCC	5280
Db	5221	CCCGGCTTCCAGGCACTACCCCAAGTAACATGACTCTCTCTGAAAATATGACTGTGCC	5280
Qy	5281	GTGGGCTTTGGAGCTCAATCCAGTCCGTGAACCTTCCACCGAGCCCAACAGACTAC	5340
Db	5281	GTGGGCTTTGGAGCTCAATCCAGTCCGTGAACCTTCCACCGAGCCCAACAGACTAC	5340
Qy	5341	ATAGAAATCCGGAATGAGGCCCTATATAGACCAAGCCGATGATGGGAAGTTCAATGGGAAC	5400
Db	5341	ATAGAAATCCGGAATGAGGCCCTATATAGACCAAGCCGATGATGGGAAGTTCAATGGGAAC	5400
Qy	5401	GAGCTTCCAAAGTCCCTCTCTCTCAACGTCACAGACCAACCGTGTATTTCCACAGCAC	5460
Db	5401	GAGCTTCCAAAGTCCCTCTCTCTCTCAACGTCACAGACCAACCGTGTATTTCCACAGCAC	5460
Qy	5461	CACTCCCAAGATTCGGCCAGAGATTCAAGCTGGAGTATCAGGCTATGAACTTCAAGAGTGC	5520
Db	5461	CACTCCCAAGATTCGGCCAGAGATTCAAGCTGGAGTATCAGGCTATGAACTTCAAGAGTGC	5520
Qy	5521	CCAGACCCAGAGCCCTTTGGCCAAATGGACATTGAGAGGGAAGCTGGCTAACATGTGGGCAA	5580
Db	5521	CCAGACCCAGAGCCCTTTGGCCAAATGGACATTGAGAGGGAAGCTGGCTAACATGTGGGCAA	5580
Qy	5581	TCAGTGAACCTTCAGATGCTCCCGGGGTATCAATTGACTGTGCCAACCCTGTCTCTACGTGT	5640
Db	5581	TCAGTGAACCTTCAGATGCTCCCGGGGTATCAATTGACTGTGCCAACCCTGTCTCTACGTGT	5640
Qy	5641	CAACATGGCAACCAACCGGAATGGGACCAACCCCTGCCCACAAATGTGAATGCCCTTGTGGC	5700

[illegible]

QY 6781 GGCAAGAGTACACAGTGGGAACCAAGGCCGNGTACAGCTGCAGTGAAGGCTACCACTTC 6840  
Db 6552 GGCAAGAGTACACAGTGGGAACCAAGGCCGNGTACAGCTGCAGTGAAGGCTACCACTTC 6651  
QY 6841 CAGGAGGCGCTGAGAGCCACTGACAGTGTCTGACACAGGCGCTATGAGCAACCGCAAT 6900  
Db 6652 CAGGAGGCGCTGAGAGCCACTGACAGTGTCTGACACAGGCGCTATGAGCAACCGCAAT 6711  
QY 6901 GTCCCAACACAGTGTGTCTCTGTGACTTGTCTGATGTGAGTGAATCAACGCTGAGCAAT 6960  
Db 6712 GTCCCAACACAGTGTGTCTCTGTGACTTGTCTGATGTGAGTGAATCAACGCTGAGCAAT 6771  
QY 6961 GGCCCAATGAGGCGCTATCTTTGAGACACAGTATCAAGTTCAGAGCCCAAGTGAATGCTATC 7020  
Db 6772 GGCCCAATGAGGCGCTATCTTTGAGACACAGTATCAAGTTCAGAGCCCAAGTGAATGCTATC 6831  
QY 7021 TGTGACCCGTACTACTATCTGAGCCAAAGGCTCATCCGCTGTCAAGCCAAATGSCAAA 7080  
Db 6832 TGTGACCCGTACTACTATCTGAGCCAAAGGCTCATCCGCTGTGTCAAGCCAAATGSCAAA 6891  
QY 7081 TGTGACCCGTGAGGACTCTACGCCCCACCTGCGCAATCATCTCTGTGAGAGCTCCGAT 7140  
Db 6892 TGTGACCCGTGAGGACTCTACGCCCCACCTGCGCAATCATCTCTGTGAGAGCTCCGAT 6951  
QY 7141 CCCCCCAATGAGCCACCGCACTGAGAAACATGTGTCTACGAGGCAACAGCCATCTTCTCC 7200  
Db 6952 CCCCCCAATGAGCCACCGCACTGAGAAACATGTGTCTACGAGGCAACAGCCATCTTCTCC 7011  
QY 7201 TGTCAATTCGAGATACACACTGTGTGAGCTTCAGAGGTGCGTGAATGATGAGCCAAATGAGCTC 7260  
Db 7012 TGTCAATTCGAGATACACACTGTGTGAGCTTCAGAGGTGCGTGAATGATGAGCCAAATGAGCTC 7071  
QY 7261 TGTGAGTGTCTGAAAGTCCGCTGCTGTGCTGAGCACTGTGAGGACTCTGAGCCATTTGTC 7320  
Db 7072 TGTGAGTGTCTGAAAGTCCGCTGCTGTGAGCACTGTGAGGACTCTGAGCCATTTGTC 7131  
QY 7321 AACGGAACATCAATGAGGAGAACTACAGCTACCGGAGGAGTGTGATGATGATGATGATGATGAT 7380  
Db 7132 AACGGAACATCAATGAGGAGAACTACAGCTACCGGAGGAGTGTGATGATGATGATGATGATGAT 7191  
QY 7381 GCTGTGCTCCGCTGATGCGGCAATGTCTGTGCGCAATCTGCGACAGAGATCATCACTGTGCTG 7440  
Db 7192 GCTGTGCTCCGCTGATGCGGCAATGTCTGTGCGCAATCTGCGACAGAGATCATCACTGTGCTG 7251  
QY 7441 GGCAAGACCCCTTTCTGTGTGCAATTAATCTGTGACACCCAGGCAACCTGTCAACGCGC 7500  
Db 7252 GGCAAGACCCCTTTCTGTGTGCAATTAATCTGTGACACCCAGGCAACCTGTGTCAACGCGC 7307  
QY 7501 CTCACTCAAGGATACCAAGTTAACTCAACGATGTGATGATGATGATGATGATGATGATGATGAT 7560  
Db 7308 CTCACTCAAGGATACCAAGTTAACTCAACGATGTGATGATGATGATGATGATGATGATGATGAT 7367  
QY 7561 TATATGTGAGAGGAGGCTGTGATGCTCCATGCTGCGACAGGCGCAATGAGTGAATG 7620  
Db 7368 TATATGTGAGAGGAGGCTGTGATGCTCCATGCTGCGACAGGCGCAATGAGTGAATG 7427  
QY 7621 CTGCGCACTGTGAGATCATCACTGTGACATCTGTGACACCAAGAAATAGTGTGCT 7680  
Db 7428 CTGCGCACTGTGAGATCATCACTGTGACATCTGTGACACCAAGAAATAGTGTGCT 7487  
QY 7681 CAGGTGACAGGAGGAGGCGCGCAAGGTTCAAGTTCAGGACACAGTGTCTTAACGGGTGC 7740  
Db 7488 CAGGTGACAGGAGGAGGCGCGCAAGGTTCAAGTTCAGGACACAGTGTCTTAACGGGTGC 7547  
QY 7741 AACCAAGGCTTACTCTCTGTGAGCAACCCAGTGTCAAGTGTCAAGGAGATGSCAATG 7800  
Db 7548 AACCAAGGCTTACTCTCTGTGAGCAACCCAGTGTCAAGTGTCAAGGAGATGSCAATG 7607  
QY 7801 GACCGTCCCGCGCCCAAGTGTCT 7852  
Db 7608 GACCGTCCCGCGCCCAAGTGTCT 7667

QY 7853 CGCTCACTCCAGATGCTGAGACAGATTATCTGTGAGAGAGTGTGCGGTACAGCT 7912  
Db 7668 CGCTCACTCCAGATGCTGAGACAGATTATCTGTGAGAGAGTGTGCGGTACAGCT 7727  
QY 7913 GCATCGGCAAGCTGATCTGTGTGAGAAACAGACACCCGATGTGTGAGTGAATGACT 7972  
Db 7728 GCATCGGCAAGCTGATCTGTGTGAGAAACAGACACCCGATGTGTGAGTGAATGACT 7787  
QY 7973 GGAATGCTCCCTCCCTCACTGTGTGAGAAACAGACACCCGATGTGTGAGTGAATGACT 8032  
Db 7788 GGAATGCTCCCTCCCTCACTGTGTGAGAAACAGACACCCGATGTGTGAGTGAATGACT 7847  
QY 8033 TCCGCGCTCATGAGATCGATGTGTGAGAAACAGCTTGTATCCAGGACATGTGATGAGCTTCA 8092  
Db 7848 TCCGCGCTCATGAGATCGATGTGTGAGAAACAGCTTGTATCCAGGACATGTGATGAGCTTCA 7907  
QY 7908 GCTGTGAAGCTGGCCAGTGTCTCCGAGGATGTGAGAGCGACCTGTCAACCAATGAGCT 7967  
QY 8153 CGTGAAGGCGCTGAGAGCTGAGTGTGAGATCTCTGTGAGAAACCCGTGAGCTCCAA 8212  
Db 7968 GCTGTGAAGCTGGCCAGTGTCTCCGAGGATGTGAGAGCGACCTGTCAACCAATGAGCT 7967  
QY 8213 GTATAGCCGAGTGTGTGATGATGAGGCTGTGTGTCTCCAGCTTATCGTCTATGAGT 8272  
Db 8028 GTATAGCCGAGTGTGTGATGATGAGGCTGTGTGTCTCCAGCTTATCGTCTATGAGT 8087  
QY 8273 GCGGGAAGATGATGAGGCAACAGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 8332  
Db 8088 GCGGGAAGATGATGAGGCAACAGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 8147  
QY 8333 GGAAGAGAGTGAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 8392  
Db 8148 GGAAGAGAGTGAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 8207  
QY 8393 ATGAGCTTCCGCTGAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8452  
Db 8208 ATGAGCTTCCGCTGAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8267  
QY 8453 CTGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8512  
Db 8268 CTGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8327  
QY 8513 GGAATGGAACCAAGCCGCTGCAAAAGCTGCAATGAGTGAACCAAGCCGCTGCAATGAGTGA 8572  
Db 8328 GGAATGGAACCAAGCCGCTGCAAAAGCTGCAATGAGTGAACCAAGCCGCTGCAATGAGTGA 8387  
QY 8573 ATGGAAGAGTGTGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8632  
Db 8388 ATGGAAGAGTGTGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8447  
QY 8633 AGGAGTACAGCTTCTCTGCGCGCGGCTTCACTGTGAGAGAAATGAGTCTGAGACCG 8692  
Db 8448 AGGAGTACAGCTTCTCTGCGCGCGGCTTCACTGTGAGAGAAATGAGTCTGAGACCG 8507  
QY 8693 GAGAGTCCCTCAATGTTTCTCTGTGTTCTGCGGAGAACTGTGAGTCCCGTCCGTTGGA 8752  
Db 8508 GAGAGTCCCTCAATGTTTCTCTGTGTTCTGCGGAGAACTGTGAGTCCCGTCCGTTGGA 8567  
QY 8753 GGAAGAGAGACGAGAGCTTCTCTACAGTATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8812  
Db 8568 GGAAGAGAGACGAGAGCTTCTCTACAGTATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8627  
QY 8813 TGTGTGTGTGAGGCTTCTCTACAGTATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8872  
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Db      8748 GGATACAGAAACATTCTCAGGGGTACAGAGTTGAAAGCAAGTCCCTCCCTGTCACAA 8807
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Qy      9893 AATGTAAGACCGCAATCCAGCCACAGACATCATGGCCAGGAGCGGAGTTTCAAGT 9952
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Qy      9953 CAGCAAGTGTGACAGCAGTATAGCCACCGGCTGGCGGCTTTTTTGTAGTTGAA 10012
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Qy      10133 CCAC 10136
Db      9948 CCAC 9951

RESULT 6
ADH71135
ID ADH71135 standard; DNA; 10655 BP.
AC ADH71135;
DT 25-MAR-2004 (first entry)
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DE Human gene of the invention NOV4a SEQ ID NO:31.
KW ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antihypertensive; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN W02003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
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PR 05-JUN-2002; 2002US-0386041P.
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PR 14-JUN-2002; 2002US-0389146P.
PR 14-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.

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QY	1061	AAGAGGAATTATGGCAACACACTCCATCTGTGTCTGGCTCATCTCTGGCCAGGCTTAAGAGCC	1120
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QY	1121	GCATTCACCTGGCCTTCAACGACATTTGACGATGGAGCCCTCAGTTTGATTTCTGTGTCATCA	1180
DB	1778	GCATTCACCTGGCCTTCAACGACATTTGACGATGGAGCCCTCAGTTTGATTTCTGTGTCATCA	1837
QY	1181	AGGATGGGGCCACCGCCGAGGGCCGCCGTCTGGGGCACCTTCTCAGAAACCAGTTCCCT	1240
DB	1838	AGGATGGGGCCACCGCCGAGGGCCGCCGTCTGGGGCACCTTCTCAGAAACCAGTTCCCT	1897
QY	1241	CCTCCATCAACAAGCAGTGGCCACGATGGCCGCTCTGAGTTTCAAGATCTGACATCTCCACAG	1300
DB	1898	CCTCCATCAACAAGCAGTGGCCACGATGGCCGCTCTGAGTTTCAAGATCTGACATCTCCACAG	1957
QY	1301	GGAAAGAGGGGCTTCAACATCACTTTTACACCTTCCGACCAAGAGAGGCCCGGATCCCTG	1360
DB	1958	GGAAAGAGGGGCTTCAACATCACTTTTACACGATGACTCTCCAAAGAGTCCCGGATCCCTG	2017
QY	1361	GCGTTCCAGTAAATGGCAAAACGGTTTGGGGACAGCCTTCCAGCTGGGCAAGCTCCATCTCT	1420
DB	2018	GCGTTCCAGTAAATGGCAAAACGGTTTGGGGACAGCCTTCCAGCTGGGCAAGCTCCATCTCT	2077
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DB	2078	TCCTCTGTGATGAAAGGCTTCTTGGGATCTCAGGGCTCAGAGACATCACTCGCTCCTGA	2137
QY	1481	AGGAGGGGAGGGTGTCTGGAACAGCGCTGATGCGGTGTGAAAGTCCCTGTGTGTGTC	1540
DB	2138	AGGAGGGGAGGGTGTCTGGAACAGCGCTGATGCGGTGTGAAAGTCCCTGTGTGTGTC	2197
QY	1541	ACCTGACTTGCGCCAGCGGCAACATCTCTCTCGGGGCTGGCCTTGCTTCAACAAGATG	1600
DB	2198	ACCTGACTTGCGCCAGCGGCAACATCTCTCTCGGGGCTGGCCTTGCTTCAACAAGATG	2257
QY	1601	CCTTGAGCTGTGCTGGGTGATTGAGGCCACGCGAGCTTACCCATCAAAATCACTTTCG	1660
DB	2258	CCTTGAGCTGTGCTGGGTGATTGAGGCCACGCGAGCTTACCCATCAAAATCACTTTCG	2317
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DB	2318	ACAGATTCAAAAACGAGGTCAACTATGACACCTCTGGAAGTACGGGATGGGGGCACTTACT	2377
QY	1721	CAGCGCCCTTGATCGGGGTTTACACGCGGAGCCAGAGTTCCCAAGTTCTCTATCAGACCA	1780
DB	2378	CAGCGCCCTTGATCGGGGTTTACACGCGGAGCCAGAGTTCCCAAGTTCTCTATCAGACCA	2437
QY	1781	GCAACTACCTTCACTCTCTTCTTCAACGACAAAGATCACTGTGGAGCATCGGCTTCCAGC	1840
DB	2438	GCAACTACCTTCACTCTCTTCTTCAACGACAAAGATCACTGTGGAGCATCGGCTTCCAGC	2497
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DB	2498	TCCGCTAATGAACTTTAACACTGCAAGTCAACACTGTCTGGATTCAGAAATCCCACTTAA	2557
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DB	2558	ATGGAACAGCTCATGGGAATGACTTTCACTGATGGGGCGCTGGTAGCTTTCAGCTGTGACT	2617
QY	1961	CGGGCTACACATTAAGTACGCGGAGACCTCTGGAATGTAGCCCACTTCCAGTGAAGCC	2020
DB	2618	CGGGCTACACATTAAGTACGCGGAGACCTCTGGAATGTAGCCCACTTCCAGTGAAGCC	2677
QY	2021	GGGCGCTTCCAGTTGTGAAGCTCTCTGTGGTGTATTATTCAGAGGCTCCAGTGGAGCA	2080
DB	2678	GGGCGCTTCCAGTTGTGAAGCTCTCTGTGGTGTATTATTCAGAGGCTCCAGTGGAGCA	2737
QY	2081	TCTTGTGCGCAGGGTTCCCTGACTTTCAACCCCAACAACTTGAATGCACTGGAATTATCG	2140
DB	2738	TCTTGTGCGCAGGGTTCCCTGACTTTCAACCCCAACAACTTGAATGCACTGGAATTATCG	2797
QY	2141	AAACATCTCATGGCAAGGGATGTGTTCTTCACTTTCACACCTTCCAGCTGGAAAGTGGCC	2200

Dp	2798	AAACATCTCATGCGAAGGGATGTTCTTCACTTTCACACCTTCCACTGGAAAGTGGCC	2857
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Dp	2858	ATGACTACTCCTCATCACTAGAGAACGGCAGCTTCACCCAGCCCTGAGGCGATTAATG	2917
Qy	2261	GATCTCGGCTGCCAGCTCCCATCAAGCGCTGGGGCTCTATGGCACTTCACTGCCAGTTC	2320
Dp	2918	GATCTCGGCTGCCAGCTCCCATCAAGCGCTGGGGCTCTATGGCACTTCACTGCCAGTTC	2977
Qy	2231	GCTTCATCTCGATTTCTCCATGTCATATGAAAGGATTCACATCACTTCACAGATACG	2380
Dp	2978	GCTTCATCTCGATTTCTCCATGTCATATGAAAGGATTCACATCACTTCACAGATACG	3037
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Dp	3038	ACTTGSAGCCCTGTGAGAGAGCCCGAGGCTCCAGAGCTACAGATCCGGAAAGGCTTTGAGT	3097
Qy	2441	TTGGGCTGGGCGACACTTGACTTTCCTTCCTGCTTCCCGGGATCCGTTGTGAGGGCACCG	2500
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Dp	3218	TTGCTGAGTGTGGGAATTCACTCAACAGGCACTCAAGGATCTTTGCTGTCGCCCAACTTTC	3277
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Dp	3278	CTGTGAATCAATTAACATCATGATGATGATCTTACTCCATCCAGACCAGCCAGGAGAGG	3337
Qy	2681	GAATTCACTGAAAGCCAGGGCACTTCCAACTCTCCGAAGGAGATGCTCTCAAGTTTATG	2740
Dp	3338	GAATTCACTGAAAGCCAGGGCACTTCCAACTCTCCGAAGGAGATGCTCTCAAGTTTATG	3397
Qy	2741	ATGGCAACAAACACTCCGCCGCTTGGCTGGGGAGTTTATTAAGCACTTCTGAGATGATGGGGG	2800
Dp	3398	ATGGCAACAAACACTCCGCCGCTTGGCTGGGGAGTTTATTAAGCACTTCTGAGATGATGGGGG	3457
Qy	2801	TGACTTTGAACAGACATCCAGCAGTCTGTGGCTTGAATTCATCACTGATGCTGAAAAA	2860
Dp	3458	TGACTTTGAACAGACATCCAGCAGTCTGTGGCTTGAATTCATCACTGATGCTGAAAAA	3517
Qy	2861	CCAGCAAGGCTTTGAACCTGCACTTTTCAGCTTTGAACTCATCAAAATGTGAGAACCCAG	2920
Dp	3518	CCAGCAAGGCTTTGAACCTGCACTTTTCAGCTTTGAACTCATCAAAATGTGAGAACCCAG	3577
Qy	2921	GAACCCCCCAATTTGGGCTACAAAGGTATATGTAAGGTCATTTTGACGGGAGCTCCGAT	2980
Dp	3578	GAACCCCCCAATTTGGGCTACAAAGGTATATGTAAGGTCATTTTGACGGGAGCTCCGAT	3637
Qy	2981	CCTTCAGCTGTGACCTCTGATACAGCTCGCGGTAGTGAAGAGACTGCTGTGTCTGATG	3040
Dp	3638	CCTTCAGCTGTGACCTCTGATACAGCTCGCGGTAGTGAAGAGACTGCTGTGTCTGATG	3697
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 QY 5795 CCATTGGCCATGGCGGTCCGCTCAACCTCAGCGCTGTGAGAGAGAGCCCTGTGAGATT 5854  
 DB 6458 CCATTGGCCATGGCGGTCCGCTCAACCTCAGCGCTGTGAGAGAGAGCCCTGTGAGATT 6517  
 QY 5855 TCATCAACATCTGGAGTGGGCAACAGCAACAGCAACGAGCTGGGCTTTCAACCCGGA 5914  
 DB 6518 TCATCAACATCTGGAGTGGGCAACAGCAACAGCAACGAGCTGGGCTTTCAACCCGGA 6577  
 QY 5915 GCATGGCAAGAAACAGTGCAGATTCATCAACAGGCTCCGCTCAATTCACACCGTG 5974  
 DB 6578 GCATGGCAAGAAACAGTGCAGATTCATCAACAGGCTCCGCTCAATTCACACCGTG 6637  
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 DB 6698 CTCTCCCAACATCTCTCCCAACGCGGAGTCTGCACAGAAATGAAGAAATTCATATAG 6757  
 QY 6095 GTGCAATCGTACGCTACAGATGCCTCCGCTTATCCTTAGTGGGAAATGAATTTCTGA 6154  
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 QY 6215 GTTCAACAAATGAGCTTCTGACAGACTCAACAGGCTGATCTGAGCCAGAGCTTACCTG 6274  
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 QY 6275 GAGGCAATCCCGGATTCAGAACTGCTGTGGCTGGTGGAGAGTGGAGCCGCAATTAATCA 6334  
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 DB 7238 TCCATGGCTTATCTTATAGGCAACAGCAACCAAGCCCGGGGGCTCATCTACTTTGGCT 7297  
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 QY 7175 TCTAGGGGGCAACAGCATCTTCTCTGCAATTCGGGATTAACACATGAGGGGCTTCAAGG 7234  
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 DB 8198 TGGTCAAGTTTGTGCAACCCCTGGGTATATGAGTGAAGGGGCTGTAGTCCCAATGGC 8257  
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QY 7655 CTGGACACCAAGAAAATAGTGTTCGTAGGTCCAGCCGACGCGGCCGCAAGATTACGT 7714  
Db 8318 CTGGACACCAAGAAAATAGTGTTCGTAGGTCCAGCCGACGCGGCCGCAAGATTACGT 8377  
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Db 8438 TCAAGTCCAGAGGAGATGGCACTGGGACCGTCCCGCCCAAGTGTCTTGTGTCTT 8497  
QY 7835 GTGGACATCCGGGCTCCCGGCTCATCTCCAGATGTCTGAGACAGTTATCTGTGGGAG 7894  
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Db 8678 TTTCGCGTACCCCTGAGGATCCCGGCTCATGGCACTCCGTTTGGGGGACAGCTTGTATCCAG 8737  
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QY 8735 GTGTCCCGTCCCGTGGGAGAGAGGACCGAGGCTTCTCTACAGGTCATCTGTCTCT 8794  
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QY 9035 CAAACCTGACCTGGAGTGGAAACCCACCTGACTGTTCCTCCACACACTGACAGGCCAG 9094  
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QY 9214 CGGATGCGAGTGTGACAGGACGCGCCCATCTGCTGTGAGTGTGCGGCCAGTGGAGAC 9273  
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 DB 10478 ACAGAGAAAGACCCAAAGTTCTTTCAATGGCTATGCGCCAGAGAAACACCAATGTTTC 10537  
 QY 9874 GGGCCACATTGTGAAACCCCAATGTACGACCGCAACATCCAGCCCAACAGACATATGGCCA 9933  
 DB 10538 GGGCCACATTGTGAAACCCCAATGTACGACCGCAACATCCAGCCCAACAGACATATGGCCA 10597  
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 DB 10598 GCGAGGCGAGATTACAGATGACAGACAGTATAGCCAGCCGCGCTGGC 10655

RESULT 7  
 ADH71143  
 ID ADH71143 standard; DNA; 10466 BP.  
 AC ADH71143;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Human gene of the invention NOVae SEQ ID NO:39.  
 XX  
 KW db; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;  
 KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;  
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
 KW obesity; diabetes; infectious disease; metabolic syndrome X;  
 KW dyslipidemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003102155-A2.  
 XX  
 PD 11-DEC-2003.  
 XX  
 XX 03-JUN-2003; 2003WO-US017430.  
 PF  
 PR 03-JUN-2002; 2002US-0385120P.  
 PR 04-JUN-2002; 2002US-0385784P.  
 PR 05-JUN-2002; 2002US-0386041P.  
 PR 05-JUN-2002; 2002US-0386047P.  
 PR 06-JUN-2002; 2002US-0386376P.  
 PR 06-JUN-2002; 2002US-0386453P.  
 PR 06-JUN-2002; 2002US-0386644P.  
 PR 06-JUN-2002; 2002US-0387016P.  
 PR 07-JUN-2002; 2002US-0386796P.  
 PR 07-JUN-2002; 2002US-0386816P.  
 PR 07-JUN-2002; 2002US-0386931P.  
 PR 07-JUN-2002; 2002US-0386942P.  
 PR 07-JUN-2002; 2002US-0386971P.  
 PR 07-JUN-2002; 2002US-0387262P.  
 PR 08-JUN-2002; 2002US-0296960P.  
 PR 10-JUN-2002; 2002US-0387400P.  
 PR 10-JUN-2002; 2002US-0387535P.  
 PR 11-JUN-2002; 2002US-0387610P.  
 PR 11-JUN-2002; 2002US-0387625P.  
 PR 11-JUN-2002; 2002US-0387634P.  
 PR 11-JUN-2002; 2002US-0387688P.  
 PR 11-JUN-2002; 2002US-0387696P.  
 PR 11-JUN-2002; 2002US-0387702P.  
 PR 11-JUN-2002; 2002US-0387836P.  
 PR 11-JUN-2002; 2002US-0387859P.  
 PR 12-JUN-2002; 2002US-0387933P.  
 PR 12-JUN-2002; 2002US-0387934P.  
 PR 12-JUN-2002; 2002US-0387960P.  
 PR 12-JUN-2002; 2002US-0388022P.  
 PR 12-JUN-2002; 2002US-0388096P.  
 PR 13-JUN-2002; 2002US-0389123P.  
 PR 14-JUN-2002; 2002US-0389188P.  
 PR 14-JUN-2002; 2002US-0389170P.  
 PR 14-JUN-2002; 2002US-0389144P.  
 PR 14-JUN-2002; 2002US-0389146P.  
 PR 17-JUN-2002; 2002US-0389729P.

PR 17-JUN-2002; 2002US-0389742P.  
 PR 18-JUN-2002; 2002US-0389808P.  
 PR 19-JUN-2002; 2002US-0390064P.  
 PR 19-JUN-2002; 2002US-0390209P.  
 PR 21-JUN-2002; 2002US-0390763P.  
 PR 17-JUL-2002; 2002US-0396706P.  
 PR 06-AUG-2002; 2002US-0401628P.  
 PR 09-AUG-2002; 2002US-0402156P.  
 PR 09-AUG-2002; 2002US-0402256P.  
 PR 09-AUG-2002; 2002US-0402389P.  
 PR 12-AUG-2002; 2002US-0402786P.  
 PR 12-AUG-2002; 2002US-0402816P.  
 PR 12-AUG-2002; 2002US-0402821P.  
 PR 12-AUG-2002; 2002US-0402832P.  
 PR 13-AUG-2002; 2002US-0403448P.  
 PR 13-AUG-2002; 2002US-0403532P.  
 PR 13-AUG-2002; 2002US-0403531P.  
 PR 13-AUG-2002; 2002US-0403532P.  
 PR 13-AUG-2002; 2002US-0403563P.  
 PR 13-AUG-2002; 2002US-0406317P.  
 PR 15-AUG-2002; 2002US-0406317P.  
 PR 26-AUG-2002; 2002US-0406182P.  
 PR 26-AUG-2002; 2002US-0406355P.  
 PR 27-AUG-2002; 2002US-0406240P.  
 PR 12-SEP-2002; 2002US-0410084P.  
 PR 20-SEP-2002; 2002US-0412528P.  
 PR 23-SEP-2002; 2002US-0412731P.  
 PR 30-SEP-2002; 2002US-0414801P.  
 PR 30-SEP-2002; 2002US-0414839P.  
 PR 30-SEP-2002; 2002US-0414840P.  
 PR 30-SEP-2002; 2002US-0414954P.  
 PR 09-OCT-2002; 2002US-0417186P.  
 PR 09-OCT-2002; 2002US-0417406P.  
 PR 23-OCT-2002; 2002US-0420639P.  
 PR 28-OCT-2002; 2002US-0421156P.  
 PR 31-OCT-2002; 2002US-0422690P.  
 PR 01-NOV-2002; 2002US-0423130P.  
 PR 05-NOV-2002; 2002US-00423798.  
 PR 05-NOV-2002; 2002US-0423798P.  
 PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.  
 XX  
 PA  
 XX  
 PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;  
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
 PI Rutenberg S, Gangoli BA, Gerlach VR, Gorman L, Gunther E, Guo X;  
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR,  
 PI MacIsaac T, Malyankar UM, Mezick AJ, Mallet I, Mishra VS;  
 PI Padigar M, Patnurajan M, Pena CA, Peyman JA, Raha D, Rastell L;  
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
 PI Zhong H;  
 XX  
 DR  
 DR MPI; 2004-081935/08.  
 DR P-PDB; ADH71144.  
 XX  
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
 PT creating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
 XX  
 PS Example 4; SEQ ID NO 39; 1880pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide (NOVX). A  
 CC polypeptide of the invention has cytosolic, immunomodulator,  
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
 CC antilipemic activity, and may have a use in gene therapy, and as a  
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
 CC any of the 303 fully defined nucleotide sequences given in the  
 CC specification. The polypeptide is useful in the manufacture of a  
 CC medicament for treating a syndrome associated with a human disease. The  
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
CC further used as hybridisation probes, in chromosome mapping, tissue  
CC typing, preventive medicine, and pharmacogenomics. The present sequence  
CC encodes a NOVX polypeptide of the invention.

XX Sequence 10466 BP; 2222 A; 3160 C; 2832 G; 2252 T; 0 U; 0 Other;

Query Match 90.0%; Score 9120; DB 12; Length 10466;  
Best Local Similarity 96.1%; Pred. No. 0;  
Matches 9513; Conservative 0; Mismatches 105; Indels 280; Gaps 5;

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QY 101 AGCTAGTCAAGAAAGCAATTTAGTTGAAGTCTCGAGGTGTGAAGCTGATGCCAGCAAG 160
DB ACCAATGCAAGAAAGCAATTTAGTTGAAGTCTCGAGGTGTGAAGCTGATGCCAGCAAG 901
QY 161 ACAACAGCCAGAAAGAGTGTGTCTTAACATGAGTTGTGTCTCCAGACATATATCT 220
DB ACAACAGCCAGAAAGAGTGTGTCTTAACATGAGTTGTGTCTCCAGACATATATATCT 961
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DB GTCCAGACCTGGCATACCCGAAAGAGGCAAAAGACTAGGCTCGATTTCAAGTTAGAT 1021
QY 281 CCAGCGTCCAGTTACCTGCAACGAGGCTATGACCTGCAAGGCTCAAGCGATCACCT 340
DB CCAGCGTCCAGTTACCTGCAACGAGGCTATGACCTGCAAGGCTCAAGCGATCACCT 1081
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DB GATATGAATGAGCCGACATGTTTGGCGCTCGAGGACACACAGGCCAGTCTCCAGACCC 1141
QY 401 GCATGTGTATGCCCACTTTCGAGGCGCTCGAGGCTATGACCTGCAAGGCTCAAGGCT 460
DB GCATGTGTATGCCCACTTTCGAGGCGCTCGAGGCTATGACCTGCAAGGCTCAAGGCT 1201
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QY 701 GGCAGAAATGACGTGATCTGATCTGTCTGACATTTAGCACTTCAATGCAAGTCAAG 760
DB GGCAGAAATGACGTGATCTGATCTGTCTGACATTTAGCACTTCAATGCAAGTCAAG 1417
QY 761 GTTCAAGTGAAGAGTCTCCAAAGACTTCTAATGCTGTGGAATTGTTGCTCTCGGACAG 820
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QY 8075 GCACTGTATGGCTTCACTGTGAAGCTGGGCAAGTGTCTCCGGGATGTGACAGCCGA 8134  
DB 8549 GCACTGTATGGCTTCACTGTGAAGCTGGGCAAGTGTCTCCGGGATGTGACAGCCGA 8608  
QY 8135 CCTGTCAACCAATGGCTGTGGAGGCGCTCGAGGCTGAGTGTGAGTGTCTGTG 8194  
DB 8609 CCTGTCAACCAATGGCTGTGGAGGCGCTCGAGGCTGAGTGTGAGTGTCTGTG 8668  
QY 8195 GGAACCTTGGGACTCCAGATTAATGCCGAGTTGTGTGATGATGAGCTGTGTTCTCA 8254  
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DB 8729 GCTCTATGCTTATGATGCTCCGGAAGATTAATGCGCACAGGCTGCTCAGCCGTCACT 8788  
QY 8315 GCTCGGTCAATGGTATCTGGACAGGAGTGAACCTGAGTGGCTCGCATTAAGTGTG 8374  
DB 8789 GCTCGGTCAATGGTATCTGGACAGGAGTGAACCTGAGTGGCTCGCATTAAGTGTG 8848  
QY 8375 ACCCTGGGATTCAGGCAATGGGCTTCCGCTGGGCAATGATCTTCAAGGTCAACAAAAC 8434  
DB 8849 ACCCTGGGATTCAGGCAATGGGCTTCCGCTGGGCAATGATCTTCAAGGTCAACAAAAC 8908  
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DB 8909 TGAATATAGTGTGTCTCTGCTATATGATGAGTCAATAGAGTATCTGTGAGCT 8968  
QY 8495 GCACCAAGGACCGGACATGGAATGGAACCAAGCCGCTGCAAAAGCTCATGTGCAAC 8554  
DB 8969 GCACCAAGGACCGGACATGGAATGGAACCAAGCCGCTGCAAAAGCTCATGTGCAAC 9028  
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QY 8675 GAAATGGGTCTGGAACCGGAGAGCTGCTCAAGTGTTCCTGTGTCTCGGGGATCTG 8734

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Db      9149 GAAATGGGTCCTGGACCGGAGAGTGCTCCAGTGTTCCTGTGTCTGCGGGAGTCTCG 9208
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Db      9209 GTGTCCCGTCCCGTGGAGAGAGAGACCCAGGCTTCTCTCAACGATCATCTGTCTCT 9268
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Db      9269 TCTCTGACATCCCGCTGTGTGCTGTGTGGGCTTCCAGGAGTTTGGCCAGTAG 9328
Qy      8855 GGACATGAGTGGACCCAGGCCAGCTGATAGATCCGACCTGACCAAGTGTGGAGC 8914
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Qy      8915 CTGTGTGTCACAGTTTGGGATACAGAACATTTCTCAGGGCTACCAAGTTGGAGCACAG 8974
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Db      9869 TCAGAGTGACTGGCTTCCAAAGTTGCCAACAGAGGTCAATGCAATGATGACACA 9928
Qy      9454 GTGGGTGAGAGCTGCACTTGGCTGGAACCTTAACAAGAAATTTTCTCTCTACTCC 9513
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Qy      9694 AGTCAGACCCGAGATCATTTGGCGGCACTTTGCTTCAACAGAGCTCAGTGGAGCGG 9753
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Qy      9754 CGATCTGTGCTTTTCAATGCGCCTCATTAATGCGGGCTTGTGCTATCTTCAAAAC 9813

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Db      10229 CGATCTGTGCTCTTTCATGCGCCCTCATTAATGCGGGCTTGTGCTATCTTCAAGC 10288
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Db      10289 ACAGAGAGAGACCCAAAGTTCTTTCAATGAGCTATGCTGGCCAGAGAACCAATGTTTC 10348
Qy      9874 GGGCCACATTTTGAAGACCCCAATGATGACGCAACATCCAGCCCAAGACATCATGCGCA 9933
Db      10349 GGGCCACATTTTGAAGACCCCAATGATGACGCAACATCCAGCCCAAGACATCATGCGCA 10408
Qy      9934 GCGAGGCGGAGTTTACAGTCAAGCAGTGTGACAGACAGTATACCAACCCGGCTTGGC 9991
Db      10409 GCGAGGCGGAGTTTACAGTCAAGCAGTGTGACAGACAGTATACCAACCCGGCTTGGC 10466

RESULT 8
ADH71145
ID      ADH71145 standard; DNA, 12900 BP.
XX
AC      ADH71145;
XX
DT      25-MAR-2004 (first entry)
XX
DE      Human gene of the invention NOV4E SEQ ID NO:41.
XX
KW      ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
KW      anorectic; antidiabetic; antimicrobial; antileptemic; gene therapy;
KW      vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW      obesity; diabetes; infectious disease; metabolic syndrome X;
KW      dyslipidaemia.
XX
OS      Homo sapiens.
XX
PN      WO2003102155-A2.
XX
PD      11-DEC-2003.
XX
PF      03-JUN-2003; 2003WO-US017430.
XX
PR      03-JUN-2002; 2002US-0385120P.
PR      04-JUN-2002; 2002US-0385784P.
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PR      14-JUN-2002; 2002US-0389120P.
PR      14-JUN-2002; 2002US-0389144P.

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 PR 27-AUG-2002; 2002US-0406240P.  
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 PR 09-OCT-2002; 2002US-0417186P.  
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 PR 28-OCT-2002; 2002US-0421156P.  
 PR 31-OCT-2002; 2002US-0422690P.  
 PR 01-NOV-2002; 2002US-0423130P.  
 PR 05-NOV-2002; 2002US-00423798.  
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 PR 12-NOV-2002; 2002US-0425453P.  
 XX  
 BA (CURA-) CURAGEN CORP.  
 XX  
 PI Alsbjork JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ,  
 PI Catberton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K,  
 PI Eckenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X,  
 PI Gusev VV, Herrmann JU, Ji W, Kekuda R, Li L, Liu X, McDougall JR,  
 PI MacLachlan T, Malyanar UM, Mezick AJ, Millet I, Mishra VS,  
 PI Padigaru M, Paturajan M, Pena CE, Peyman JA, Raha D, Rastelli L,  
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkels RA,  
 PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M,  
 PI Zhong H;  
 XX  
 DR WPI; 2004-081935/08.  
 DR P-PSDB; ADH71146.  
 XX  
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
 XX  
 XX Example 4; SEQ ID NO 41; 1880bp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide (NOVX). A  
 CC polypeptide of the invention has cytoskeletal, immunomodulator,  
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
 CC antihypertensive activity, and may have a use in gene therapy, and as a  
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
 CC any of the 303 fully defined nucleotide sequences given in the  
 CC specification. The polypeptide is useful in the manufacture of a  
 CC medicament for treating a syndrome associated with a human disease. The  
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,

CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
 CC further used as hybridisation probes, in chromosome mapping, tissue  
 CC typing, preventive medicine, and pharmacogenomics. The present sequence  
 CC encodes a NOVX polypeptide of the invention.  
 XX  
 SQ Sequence 12900 BP; 2893 A; 3775 C; 3410 G; 2822 T; 0 U; 0 Other;  
 Query Match 86.4%; Score 8760.4; DB 12; Length 12900;  
 Best Local Similarity 94.2%; Pred. No. 0;  
 Matches 9361; Conservative 0; Mismatches 121; Indels 458; Gaps 7;  
 QY 101 AGCTACTCAAGAAAGCAATTGAGTTGAGTTCAGTGTGAAAGCTGATGCCAGCAAG 160  
 DB ACCAAGTCAGAAAGCAAAATGAGTTGAGTTGAGTGTGAAAGCTGATGCCAGCAAG 901  
 QY 161 ACAACAGCCAGAAAGAGCTGTGTAACTCAGTTGATGTGTCCAAAGACATATATATGT 220  
 DB ACAACAGCCAGAAAGAGCTGTGTAACTCAGTTGATGTGTGTCCAAAGACATATATGT 961  
 QY 902 ACAACAGCCAGAAAGAGCTGTGTAACTCAGTTGATGTGTGTCCAAAGACATATATGT 961  
 DB 902 ACAACAGCCAGAAAGAGCTGTGTAACTCAGTTGATGTGTGTCCAAAGACATATATGT 961  
 QY 221 GTCCAGACCTGACATACCCGAAAGGGGCAAAAGACTAGGCTGGAATTCAGGTTAGAT 280  
 DB GTCCAGACCTGACATACCCGAAAGGGGCAAAAGACTAGGCTGGAATTCAGGTTAGAT 1021  
 QY 962 GTCCAGACCTGACATACCCGAAAGGGGCAAAAGACTAGGCTGGAATTCAGGTTAGAT 1021  
 DB 962 GTCCAGACCTGACATACCCGAAAGGGGCAAAAGACTAGGCTGGAATTCAGGTTAGAT 1021  
 QY 281 CCAGCGTCCAGTTCACTGCAAGAGGGCTATGACCTGCAAGGGCTCCAGCGGATCACT 340  
 DB CCAGCGTCCAGTTCACTGCAAGAGGGCTATGACCTGCAAGGGCTCCAGCGGATCACT 1081  
 QY 1022 CCAGCGTCCAGTTCACTGCAAGAGGGCTATGACCTGCAAGGGCTCCAGCGGATCACT 1081  
 DB 1022 CCAGCGTCCAGTTCACTGCAAGAGGGCTATGACCTGCAAGGGCTCCAGCGGATCACT 1081  
 QY 341 GTATGAAAGTGAGCGACATGTTTGGCGGCTGAGCGACCAAGCGGATGCGGAGCC 400  
 DB GTATGAAAGTGAGCGACATGTTTGGCGGCTGAGCGACCAAGCGGATGCGGAGCC 1141  
 QY 1082 GTATGAAAGTGAGCGACATGTTTGGCGGCTGAGCGACCAAGCGGATGCGGAGCC 1141  
 DB 1082 GTATGAAAGTGAGCGACATGTTTGGCGGCTGAGCGACCAAGCGGATGCGGAGCC 1141  
 QY 401 GCATGTGTATGTCACCTTCGAGGCCCTCGGGCATCATCACTTCCCAATTTCCCA 460  
 DB GCATGTGTATGTCACCTTCGAGGCCCTCGGGCATCATCACTTCCCAATTTCCCA 1201  
 QY 1142 GCATGTGTATGTCACCTTCGAGGCCCTCGGGCATCATCACTTCCCAATTTCCCA 1201  
 DB 1142 GCATGTGTATGTCACCTTCGAGGCCCTCGGGCATCATCACTTCCCAATTTCCCA 1201  
 QY 461 TTCAGTATGACCAATGACACCTGTGTGTGATTCATCAAGACATCAACCCCTCCAAAG 520  
 DB TTCAGTATGACCAATGACACCTGTGTGTGATTCATCAAGACATCAACCCCTCCAAAG 1261  
 QY 1202 TTCAGTATGACCAATGACACCTGTGTGTGATTCATCAAGACATCAACCCCTCCAAAG 1261  
 DB 1202 TTCAGTATGACCAATGACACCTGTGTGTGATTCATCAAGACATCAACCCCTCCAAAG 1261  
 QY 521 TGATCAAGCTCGCTTTGAGAGTTGATTTGAGAGGGGCTATGACACCTTCAGGTCG 580  
 DB TGATCAAGCTCGCTTTGAGAGTTGATTTGAGAGGGGCTATGACACCTTCAGGTCG 1321  
 QY 1262 TGATCAAGCTCGCTTTGAGAGTTGATTTGAGAGGGGCTATGACACCTTCAGGTCG 1321  
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 QY 581 GTGATGTGTGTCAGATGAGGACCAAGACAGTTCTTACATGTCTCAAAATGCTGCA 640  
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QY 1001 TGTTCCTGCTTCTTCACTTCAACAGCCGCTGAGGGTGTCTGTCTCCCACTACC 1060  
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 DB 2978 GCTTCACTCTGATTTCTCCATGTCAATGAAGATCAATGACCTTCCAGATGAG 3037  
 QY 2381 ACTTGAAGCCCTGTGAGAGCCGAGGCTCCAGCTCAGCATCCGAAAGGCTTGCAGT 2440  
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 DB 3098 TTGGCGTGGGCGACCTTGAACCTTCTCTGCTTCCCGGGTACCGTTGGAGGGCACG 3157  
 QY 2501 CCCGATACAGTGTGCGGGGGGAGACGCGGCGCTGTGAGTCCGCTTGCACAGGTG 2560  
 DB 3158 CCCGATACAGTGTGCGGGGGGAGACGCGGCGCTGTGAGTCCGCTTGCACAGGTG 3217  
 QY 2561 TTGCTGAGTGTGGGAATTCAGTCAAGCACTCAGGGTACTTGTCTGTCCCACTTTC 2620  
 DB 3218 TTGCTGAGTGTGGGAATTCAGTCAAGCACTCAGGGTACTTGTCTGTCCCACTTTC 3277  
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 DB 3278 CTGTGAATTAATTAATATATGATGATGATCTACTCATTCACAGCCAGGAAAG 3337  
 QY 2681 GAATTCAGCTGAAGGCGAGGCAATTGCAACTCTCCGAAAGAGATGTCTCAAGTTTATG 2740  
 DB 3338 GAATTCAGCTGAAGGCGAGGCAATTGCAACTCTCCGAAAGAGATGTCTCAAGTTTATG 3397  
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 DB 3398 ATGGCAACAACACTCCGCGCTTGTCTGGAGATTTTATGCAATTCAGATGATGGGG 3457  
 QY 2801 TGACTTTGAACAGACATCCAGAGTCTGTGGCTTGAATTTTATCATCTGATGATAACA 2860  
 DB 3458 TGACTTTGAACAGACATCCAGAGTCTGTGGCTTGAATTTTATCATCTGATGATAACA 3517  
 QY 2861 CGAGCAAGGCTTGAATTCGACTTTTCACTTGAATGAACTGATGAAATGTAGAGACCGAG 2920  
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 DB 3638 CCTTCAAGTGTGACCTTGGATTAACAGCTTGGGGGTAAGTGAAGTCTGTGTCTGAATG 3697  
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 DB 3758 TGAAGAGAGAGTGTGGGGGAGGCTGTGACCCCGGATTCAGTCTCTATGAACAACA 3817  
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3878 TGGTGTTTGACACAGAGAGGTTTCAAGACGTGTGGCACTCTGGGATGAGGCTGTGAGA 3937  
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3938 GCGGGGTTCTGTAAGAGAGTGTGAGCCGGCCCTGCGCAAGACTTGCATAGACCT 3997  
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4298 TCATCTCTCAACCAATTAACCAAGAACTTACCAGGAGCAAGAGTGTGAGAG 4357  
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4778 TCTGCAAGAGCTCTGTGTGAGGAGCAAGTATGTGGTTTCAAGAGGAGTGTCTTCTCCCA 4837  
4178 ACTAAGCTGAGCTCTGTGTGAGGAGCAAGTATGTGGTTTCAAGAGGAGTGTCTTCTCCCA 4237  
4838 ACTAAGCTGAGCTCTGTGTGAGGAGCAAGTATGTGGTTTCAAGAGGAGTGTCTTCTCCCA 4897  
4238 ACTA--TGTGTGTGTGTGAGGAGTGTGTCTTCAAGAGGAGTGTGTCTTCAAGAGGAGTGT 4294  
4898 ACTATGT 4957

4295 AGGTTACAGAGGAGCAAGAGCACTCGAGGAGTCTTCAAGCTTCTTCTGAGGCTCCATA 4354  
4958 AGGTTACAGAGGAGCAAGAGCACTCGAGGAGTCTTCAAGCTTCTTCTGAGGCTCCATA 5017  
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DB 6038 GCCGATGATGGAGAGATTGATGAGAGAGGCTTCCAAAGCTCCCTCTCCACAGTCCC 6097  
| | | | |  
QY 5432 AGGAGACACCGGTATTTTCCACAGGACCACTCCCAAGATGGGACAGATTTCAAGCTGG 5491  
| | | | |  
DB 6098 ACAGAGACACCGGTATTTTCCACAGGACCACTCCCAAGATGGGACAGATTTCAAGCTGG 6157  
| | | | |  
QY 5492 AGATAGAGGCTATGAACTTCAAGATGGGACCAAGGCTTTGGCAATGGATGG 5551  
| | | | |  
DB 6158 AGATAGAGGCTATGAACTTCAAGATGGGACCAAGGCTTTGGCAATGGATGG 6217  
| | | | |  
QY 5552 TGAAGGAGCTGGCTCAACAGTGGGCAATCAAGTGACTTTCAGTGGCTCCGAGGATTC 5611  
| | | | |  
DB 6218 TGAAGGAGCTGGCTCAACAGTGGGCAATCAAGTGACTTTCAGTGGCTCCGAGGATTC 6277  
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QY 5612 AATTGACTGGCCACCTGTCTCTCACTGTTCACATGGACCAACCGGAACTGGAGCACCC 5671  
| | | | |  
DB 6278 AATTGACTGGCCACCTGTCTCTCACTGTTCACATGGACCAACCGGAACTGGAGCACCC 6337  
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| | | | |  
DB 6338 CCCTGCGCAAGTGTGAAGTCCCTTGTGGGAGGAACTCACTTCTTCCAAAGGCA-1GTGT 6396  
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QY 5732 ACTCCCGGAGGTTCCCTAGCCCGTACTCCAGCTCCAGGACTGTGTCTGTGATCACCG 5791  
| | | | |  
DB 6397 ACTCCCGGAGGTTCCCTAGCCCGTACTCCAGCTCCAGGACTGTGTCTGTGATCACCG 6456  
| | | | |  
QY 5792 TGGCCATTTGGCCATGGCCGCTCCGCTCTCACTCAAGCTGTGTGACAGACAGCCCTCTGGAG 5851  
| | | | |  
DB 6457 TGGCCATTTGGCCATGGCCGCTCCGCTCTCACTCAAGCTGTGTGACAGACAGCCCTCTGGAG 6516  
| | | | |  
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| | | | |  
DB 6517 ATTTCATCAACATCTGGGATGGGCGCACAGAAACAGACCAAGGCTCGGCTCTTCCACC 6576  
| | | | |  
QY 5912 GGAGCATGGCCAAAGAAACAGTGCAGAGTTTCAATCCAAAGGCTCTGTCAAGTTCCACC 5971  
| | | | |  
DB 6577 GGAGCATGGCCAAAGAAACAGTGCAGAGTTTCAATCCAAAGGCTCTGTCAAGTTCCACC 6636  
| | | | |  
QY 5972 GGTATGACAGCCACAGGGGGGATCTTGGCCATAGCTTTCTCGGCTTATCCACTACCAAT 6031  
| | | | |  
DB 6637 GGTATGACAGCCACAGGGGGGATCTTGGCCATAGCTTTCTCGGCTTATCCACTACCAAT 6696  
| | | | |  
QY 6032 GCCCTCTCCACACATCTCTCCCAACGCGGAGTGTCTACAGAGATGAAGATTTCAATA 6091  
| | | | |  
DB 6697 GCCCTCTCCACACATCTCTCCCAACGCGGAGTGTCTACAGAGATGAAGATTTCAATA 6756  
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| | | | |  
QY 6152 TGAACCTGCAAACTTGGAACTTACCTGAGTTGAAGGACCAACCCCGAATGTAAGTGC 6211  
| | | | |  
DB 6817 TGAACCTGCAAACTTGGAACTTACCTGAGTTGAAGGACCAACCCCGAATGTAAGTGC 6876  
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QY 6212 ACTGTCCAACTTGGAACTTACCTGAGTTGAAGGACCAACCCCGAATGTAAGTGC 6271  
| | | | |  
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| | | | |  
DB 6997 ACATCTCCCTCAGAGTGAAGTACTTCTCAGCGAAGAGCAATANGATGTTTGAATTT 7056  
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QY 6512 ACAATCGAAGGGCTTCAAGATTCGCTATTTCAGCCCTTACTGACGCTGCGCAGGGCTC 6571  
| | | | |  
DB 7177 ACAATCGAAGGGCTTCAAGATTCGCTATTTCAGCCCTTACTGACGCTGCGCAGGGCTC 7236  
| | | | |  
QY 6572 CACTCAGTGGCTTCACTCTAGGCGACAGACCAACCCCGGGGCTCCATCCACTTGG 6631  
| | | | |  
DB 7237 CACTCAGTGGCTTCACTCTAGGCGACAGACCAACCCCGGGGCTCCATCCACTTGG 7296  
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| | | | |  
DB 7297 GCTGCAAGCCGCGCTTACCCGCTGTGGGACACAGATGGCCATCTGTACCCGCGACCC 7356  
| | | | |  
QY 6692 AGGCTTACCACTGTGGAGCGCAAGCATCCCTCTCTGTCAAGCTCTTCTGTGGGCTTC 6751  
| | | | |  
DB 7357 AGGCTTACCACTGTGGAGCGCAAGCATCCCTCTCTGTCAAGCTCTTCTGTGGGCTTC 7416  
| | | | |  
QY 6752 CTGAGGCCCCGAGAAATGGATGGTGTGGCAAGGATACAGATGGGAAACCAAGGCG 6811  
| | | | |  
DB 7417 CTGAGGCCCCGAGAAATGGATGGTGTGGCAAGGATACAGATGGGAAACCAAGGCG 7476  
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QY 6812 TGTACAGCTGCAAGTGAAGCTTACCACTTCAAGGAGCGCTGAGGCGCACTGCAGAGTGC 6871  
| | | | |  
DB 7477 TGTACAGCTGCAAGTGAAGCTTACCACTTCAAGGAGCGCTGAGGCGCACTGCAGAGTGC 7536  
| | | | |  
QY 6872 TGGACACAGGCTTATGGAGCACCGCAATGTCCCAACAGTGTCTCTGTGACTTGTGC 6931  
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DB 7537 TGGACACAGGCTTATGGAGCACCGCAATGTCCCAACAGTGTCTCTGTGACTTGTGC 7596  
| | | | |  
QY 6932 CTGATGTCAAGATCAGCTGAGCATGGCCGATGGAGGCTTATCTTTGAGACACAGT 6991  
| | | | |  
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QY 6992 ATCAGTTTCAGGCGCCAGTGTACTGTGTGACCTTGGCTACTATATCTGGCCAA 7051  
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DB 7657 ATCAGTTTCAGGCGCCAGTGTACTGTGTGACCTTGGCTACTATATCTGGCCAA 7716  
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QY 7052 GGGTATCCGCTGTACAGGCGCAATGGCAATGGAACTCTGGGAGACTTACAGCCCACTGCC 7111  
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DB 7717 GGGTATCCGCTGTACAGGCGCAATGGCAATGGAACTCTGGGAGACTTACAGCCCACTGCC 7776  
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QY 7112 GAATCATCTCTGTGAGAGGCTCCGATTTCCGCCAATGGCGACCGCATCGGAACACTGT 7171  
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DB 7777 GAATCATCTCTGTGAGAGGCTCCGATTTCCGCCAATGGCGACCGCATCGGAACACTGT 7836  
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QY 7172 CTGTCTACGGGGCAACAGCAATCTTCTCTGCAATTCGGATACACACTGTGGGCTTCA 7231  
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DB 7837 CTGTCTACGGGGCAACAGCAATCTTCTCTGCAATTCGGATACACACTGTGGGCTTCA 7896  
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QY 7232 GGGTGGGATGTGATGGGCAATGGGCTCTGGAATGGCTCTGAAAGTCCGCTGTGCTG 7291  
| | | | |  
DB 7897 GGGTGGGATGTGATGGGCAATGGGCTCTGGAATGGCTCTGAAAGTCCGCTGTGCTG 7956  
| | | | |  
QY 7292 GACACTGTGGGACTCTGAGGCCATTGTCAACGAGACATCAATGAGGAGAACTACAGCT 7351  
| | | | |  
DB 7957 GACACTGTGGGACTCTGAGGCCATTGTCAACGAGACATCAATGAGGAGAACTACAGCT 8016  
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QY 7352 ACCGGGCAAGTGTGTATCCAAATGCAATGTGCTTCCGCTGTATGGCATGTCTGTGC 7411  
| | | | |  
DB 8017 ACCGGGCAAGTGTGTATCCAAATGCAATGTGCTTCCGCTGTATGGCATGTCTGTGC 8076  
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QY 7412 GCATCTGCACAGAGATCATCACTGTGTGGGCAAGACCCCTTCTGTGTGCAATTACT 7471  
| | | | |  
DB 8077 GCATCTGCACAGAGATCATCACTGTGTGGGCAAGACCCCTTCTGTGTGCAATTACT 8127  
| | | | |  
QY 7472 GTGACACCCAGGCAACCTGTCAACGGCTCACTCAGGGTAAACAGTTTAACCTCAAG 7531  
| | | | |  
DB 8128 ----- 8127  
| | | | |  
QY 7532 ATGTGTCAAGTTTGTGTGCAACCTGGGTATATGTGCTGAGGGGCTGTAGGTCCCAAT 7591  
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Db	8128	-----	8127
Qy	7592	GCCTGGCAGGGGCAATGAGTGCATGCTGCCACCTGACAGAAATCATCTGTACAG	7651
Db	8128	-----	8127
Qy	7652	ATCCTGGACACAAGAAATAGTGTGTGTCAGGTCCAGCGAGCGGCCGACAGATTCA	7711
Db	8128	-----	8127
Qy	7712	GCTTGGACCACTGTGTCTTACCGGTGCAACAGGCTTCTACCTCTGGGACCCGACG	7771
Db	8128	-----	8127
Qy	7772	TGCTCAGCTGCCAGGGAGATGGCAATGGGACGCTCCCCGCCCCAGTGTCTTGGTGT	7831
Db	8128	-----	8133
Qy	7832	CCTGTGGCCATCCGGGCTCCCGCTCACTCCAGATGTCTGGAGACAGTTATCTGTGG	7891
Db	8134	CTGTGGCCATCCGGGCTCCCGCTCACTCCAGATGTCTGGAGACAGTTATCTGTGG	8193
Qy	7892	GAGCAGTGTGGCGTACAGCTGCATGGCAAGCGTACTGTGTGGAAACAGCACCCGCA	7951
Db	8194	GAGCAGTGTGGCGTACAGCTGCATGGCAAGCGTACTGTGTGGAAACAGCACCCGCA	8253
Qy	7952	TGTGTGGCGTGCATGCATCTGCATGGCTCCCTCCCTCACTGTCTAGAAACAGCGTGG	8011
Db	8254	TGTGTGGCGTGCATGCATCTGCATGGCTCCCTCCCTCACTGTCTAGAAACAGCGTGG	8313
Qy	8012	GAGTTTGGCGTGCATCCCGGATCCCGGCTCATGGCATCCGTTTGGGGGACAGCTTTGATC	8071
Db	8314	GAGTTTGGCGTGCATCCCGGATCCCGGCTCATGGCATCCGTTTGGGGGACAGCTTTGATC	8373
Qy	8072	CAGGCACTGTGATGCGCTTCACTGTGAGCTGGCAAGCTGCTCCGGGATTCGTACAGC	8131
Db	8374	CAGGCACTGTGATGCGCTTCACTGTGAGCTGGCAAGCTGCTCCGGGATTCGTACAGC	8433
Qy	8132	GCACCTGTCAAGCAATGGCTCGTGGAGCGGCTTCGACGCTGAGTGTGGATGATCTT	8191
Db	8434	GCACCTGTCAAGCAATGGCTCGTGGAGCGGCTTCGACGCTGAGTGTGGATGATCTT	8493
Qy	8192	GTGGGAACTCTGGGACTCCAAAGTAATGCCGAGTGTGTTCAAGTATGGCTGTTTTCT	8251
Db	8494	GTGGGAACTCTGGGACTCCAAAGTAATGCCGAGTGTGTTCAAGTATGGCTGTTTTCT	8553
Qy	8252	CCAGCTTATCTGTATGATGTCGGGAGAGATACTAGCCACAGGCTGCTCAGCCGTC	8311
Db	8554	CCAGCTTATCTGTATGATGTCGGGAGAGATACTAGCCACAGGCTGCTCAGCCGTC	8613
Qy	8312	ACTGCTCGGTCAATGTGATCTGGACAGGCACTGAGTGCCTGTGATTAACCTGTG	8371
Db	8614	ACTGCTCGGTCAATGTGATCTGGACAGGCACTGAGTGCCTGTGATTAACCTGTG	8673
Qy	8372	GTGACCTGGGATTCAGCAATGAGCTTGGGCGGGCAATGACTTCAGGTACAAACAA	8431
Db	8674	GTGACCTGGGATTCAGCAATGAGCTTGGGCGGGCAATGACTTCAGGTACAAACAA	8733
Qy	8432	CTGTGACATATCAGTGTGCTCTGTGCTATATGATGAGTGCATAGAGTATCTGTGTCG	8491
Db	8734	CTGTGACATATCAGTGTGCTCTGTGCTATATGATGAGTGCATAGAGTATCTGTGTCG	8793
Qy	8492	GCTGCACCAAGAACCGGACATGGAATGGAACCAAGCCGCTGCAAAAGCTTCAATGTGCA	8551
Db	8794	GCTGCACCAAGAACCGGACATGGAATGGAACCAAGCCGCTGCAAAAGCTTCAATGTGCA	8853
Qy	8552	AGGCACCTCCGCTCATCCCAATGGGAAAGGTGGGGTCTGACTTCATGAGGGCTCA	8611
Db	8854	AGGCACCTCCGCTCATCCCAATGGGAAAGGTGGGGTCTGACTTCATGAGGGCTCA	8913
Qy	8612	GTGTGACATATGCTGTGCTGGAGGGGTACCAAGCTTCTCCCTGCGCGGTGTTCACTGTG	8671
Db	8914	GTGTGACATATGCTGTGCTGGAGGGGTACCAAGCTTCTCCCTGCGCGGTGTTCACTGTG	9373

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Qy	8672	AGGAAATGGGTCTCTGGAACCGGAGAGTGCCTAGTGTTCCTGTGTCTGCGGGATC	8731
Db	8974	AGGAAATGGGTCTCTGGAACCGGAGAGTGCCTAGTGTTCCTGTGTCTGCGGGATC	9033
Qy	8732	CTGTGTCCCGTCCCGTGGAGAGAGAGACCGAGGCTTCTCTACAGTCACTGTCT	8791
Db	9034	CTGTGTCCCGTCCCGTGGAGAGAGAGACCGAGGCTTCTCTACAGTCACTGTCT	9093
Qy	8792	CCTTCTCTGCAATCCCGCTCTGTGTGTGTGGCTCTCCAGCAGGTTTTGCCAGTCA	8851
Db	9094	CCTTCTCTGCAATCCCGCTCTGTGTGTGTGGCTCTCCAGCAGGTTTTGCCAGTCA	9153
Qy	8852	ATGGACATGGAATGGACCCAGCCAGCTGCATATACCGACCTGCACCACTGTGCGG	8911
Db	9154	ATGGACATGGAATGGACCCAGCCAGCTGCATATACCGACCTGCACCACTGTGCGG	9213
Qy	8912	ACCTGGTGTGCCACAGTTTGGATACAGAACATTTCTCAGGGCTACAGGTTGAAACA	8971
Db	9214	ACCTGGTGTGCCACAGTTTGGATACAGAACATTTCTCAGGGCTACAGGTTGAAACA	9273
Qy	8972	CAGTCTCTTCCGTTGTCAAAAAGCTTACTGCTTCAAGGCTCCACCAACAGGACCTGCC	9031
Db	9274	CAGTCTCTTCCGTTGTCAAAAAGCTTACTGCTTCAAGGCTCCACCAACAGGACCTGCC	9333
Qy	9032	TCCCAACCTGACCTGAGTGGAAACCCCACTGACCTGTGCTCCCACTGAGAGCAGC	9091
Db	9334	TCCCAACCTGACCTGAGTGGAAACCCCACTGACCTGTGCTCCCACTGAGAGCAGC	9393
Qy	9092	CAGAGACGCCAAGCATGTCACAGTGGGGCTCTGATTTGACCTCATAGGCTACACGC	9151
Db	9394	CAGAGACGCCAAGCATGTCACAGTGGGGCTCTGATTTGACCTCATAGGCTACACGC	9453
Qy	9152	TCAAT-TACTCTGCGAGAGGGCTTCTCCTCAAGGGTGGCTCGAGACCGACCTGCA	9210
Db	9454	TCAAT-TACTCTGCGAGAGGGCTTCTCCTCAAGGGTGGCTCGAGACCGACCTGCA	9513
Qy	9211	AGGCGGATGGCAGCTGAGCAGAGCAAGCCGCCATCTGCTGAGAGTCCGGCCAGTGGGA	9270
Db	9514	AGGCGGATGGCAGCTGAGCAGAGCAAGCCGCCATCTGCTGAGAGTCCGGCCAGTGGGA	9573
Qy	9271	GACCCATCAACACTGCGCGGAGACCAAGCTTCAAGGCTTCTCTGAGGATGTTT	9330
Db	9574	GACCCATCAACACTGCGCGGAGACCAAGCTTCAAGGCTTCTCTGAGGATGTTT	9633
Qy	9331	TTGCCAAGAAATTCCTGTGGAAAGGGGCTTATGAATACAGGGGAAAGAACAGCCACA	9390
Db	9634	TTGCCAAGAAATTCCTGTGGAAAGGGGCTTATGAATACAGGGGAAAGAACAGCCACA	9693
Qy	9391	TGCTCAGAGTGAAGTGGCTTCCAAAGTTCGCAACAGCAAGTCAATGCAATATGAGCC	9450
Db	9694	TGCTCAGAGTGAAGTGGCTTCCAAAGTTCGCAACAGCAAGTCAATGCAATATGAGCC	9753
Qy	9451	ACAGTGGCGTGGAGCTGCACTTGGCTGGAACCTTCAAGAAAGAAATTTTCACTCTAC	9510
Db	9754	ACAGTGGCGTGGAGCTGCACTTGGCTGGAACCTTCAAGAAAGAAATTTTCACTCTAC	9813
Qy	9511	TCCAGGTGATACAGATTAACAGGCTGTGAGATCTTTATGAATTAAGTTCAAGATGATC	9570
Db	9814	TCCAGGTGATACAGATTAACAGGCTGTGAGATCTTTATGAATTAAGTTCAAGATGATC	9673
Qy	9571	ACTGGGCTTTAATGATGACCATGTCTGTCAGAGTCTCCGAGGCACTTCATTAACAG	9630
Db	9874	ACTGGGCTTTAATGATGACCATGTCTGTCAGAGTCTCCGAGGCACTTCATTAACAG	9933
Qy	9631	GCTCTGTCAAGGGCCAAAGCTTGTGGCAGTTTGGCTTCAAAAGACTGACCTCAGGCTGC	9690
Db	9934	GCTCTGTCAAGGGCCAAAGCTTGTGGCAGTTTGGCTTCAAAAGACTGACCTCAGGCTGC	9993
Qy	9691	TGGAGTCAAGCCCGAGTCAATTTGCGGCACTTTTCCATCAACAGACCTCAGTGGCAG	9750
Db	9994	TGGAGTCAAGCCCGAGTCAATTTGCGGCACTTTTCCATCAACAGACCTCAGTGGCAG	10053

QY 9751 CCGGACCTGTCCTTCATCGCCCTCATTTATTCGGGCTTCGTCCTCTCTACA 9810  
 DB 10054 CCGGACCTGTCCTTCATCGCCCTCATTTATTCGGGCTTCGTCCTCTCTACA 10113  
 QY 9811 AGACAGGAGAACCCCAAGTCTTCATAGGCTATGCTGCCAGGAACCAAG 9870  
 DB 10114 AGACAGGAGAACCCCAAGTCTTCATAGGCTATGCTGCCAGGAACCAAG 10173  
 QY 9871 TTCGGGCACTTTGAGAACCAATGTACAGACCGCAACATCCAGCCAGCATCATG 9930  
 DB 10174 TTCGGGCACTTTGAGAACCAATGTACAGACCGCAACATCCAGCCAGCATCATG 10233  
 QY 9931 CCAAGCAGCGGAGATTCAAGTCAGACAGTGTGCACAGCAGTATAGCCAGCGGCTGG 9990  
 DB 10234 CCAAGCAGCGGAGATTCAAGTCAGACAGTGTGCACAGCAGTATAGCCAGCGGCTGG 10293  
 QY 9991 CCGCTTTTTCGTAGTGAATGCTGTACTCCAGGACCGG 10030  
 DB 10294 CCGCACCAACCGCACCGAGAGCCCGCTCCAGCAGCGG 10333

RESULT 9  
 ADH71139  
 ID ADH71139 standard; DNA; 8010 BP.  
 XX ADH71139;  
 AC ADH71139;  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Human gene of the invention NOV4c SEQ ID NO:35.  
 XX  
 KW ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;  
 KW anorectic; antidiabetic; antimicrobial; antileptemic; gene therapy;  
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
 KW obesity; diabetes; infectious disease; metabolic syndrome X;  
 KW dyslipidaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003102155-A2.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PF 03-JUN-2003; 2003WO-US017430.  
 PR 03-JUN-2002; 2002US-0385120P.  
 PR 04-JUN-2002; 2002US-0385784P.  
 PR 05-JUN-2002; 2002US-0386041P.  
 PR 05-JUN-2002; 2002US-0386047P.  
 PR 06-JUN-2002; 2002US-0386376P.  
 PR 06-JUN-2002; 2002US-0386453P.  
 PR 06-JUN-2002; 2002US-0386864P.  
 PR 07-JUN-2002; 2002US-0387016P.  
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 PR 08-JUN-2002; 2002US-0296960P.  
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 PR 11-JUN-2002; 2002US-0387610P.  
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 PR 12-JUN-2002; 2002US-0387934P.  
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PR 12-JUN-2002; 2002US-0388022P.  
 PR 12-JUN-2002; 2002US-0388096P.  
 PR 13-JUN-2002; 2002US-0389123P.  
 PR 14-JUN-2002; 2002US-0389118P.  
 PR 14-JUN-2002; 2002US-0389120P.  
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 PR 18-JUN-2002; 2002US-0389844P.  
 PR 19-JUN-2002; 2002US-0390006P.  
 PR 19-JUN-2002; 2002US-0390209P.  
 PR 21-JUN-2002; 2002US-0390763P.  
 PR 17-JUL-2002; 2002US-0396706P.  
 PR 06-AUG-2002; 2002US-0401628P.  
 PR 09-AUG-2002; 2002US-0402156P.  
 PR 09-AUG-2002; 2002US-0402256P.  
 PR 09-AUG-2002; 2002US-0402389P.  
 PR 12-AUG-2002; 2002US-0402786P.  
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 PR 12-AUG-2002; 2002US-0402821P.  
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 PR 13-AUG-2002; 2002US-0403459P.  
 PR 13-AUG-2002; 2002US-0403531P.  
 PR 13-AUG-2002; 2002US-0403532P.  
 PR 13-AUG-2002; 2002US-0403563P.  
 PR 13-AUG-2002; 2002US-0406317P.  
 PR 15-AUG-2002; 2002US-0406317P.  
 PR 26-AUG-2002; 2002US-0406182P.  
 PR 26-AUG-2002; 2002US-0406355P.  
 PR 27-AUG-2002; 2002US-0406240P.  
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 PR 20-SEP-2002; 2002US-0412528P.  
 PR 23-SEP-2002; 2002US-0412731P.  
 PR 30-SEP-2002; 2002US-0414801P.  
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 PR 09-OCT-2002; 2002US-0417166P.  
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 PR 23-OCT-2002; 2002US-0420639P.  
 PR 28-OCT-2002; 2002US-0421156P.  
 PR 31-OCT-2002; 2002US-0422690P.  
 PR 01-NOV-2002; 2002US-0423130P.  
 PR 05-NOV-2002; 2002US-0423798P.  
 PR 05-NOV-2002; 2002US-0423798P.  
 PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.  
 XX  
 PA  
 XX  
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 PI Albrock JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ,  
 PI Carteron E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K,  
 PI Ettenberg S, Gangoli BA, Gerlach VL, Gorman L, Gunther E, Guo X,  
 PI Guev VY, Herrmann JU, Ji W, Kekuda R, Li L, Liu X, Macdougall JR,  
 PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS,  
 PI Padigan M, Paturajan M, Pena CE, Peyman JA, Raha D, Rastelli L,  
 PI Ridger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkels RA,  
 PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M,  
 PI Zhong H;  
 XX  
 DR WPI; 2004-081935/08.  
 DR P-PSDB; ADH71140.  
 XX  
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
 PT treating NOVX-associated disorders, e.g., cancer, diabetes, infection or  
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
 XX  
 PS Example 4; SEQ ID NO 35; 1880Pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide (NOVX). A  
 CC polypeptide of the invention has cytosolic, immunomodulator,  
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

CC antipneumatic activity, and may have a use in gene therapy, and as a  
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
 CC any of the 303 fully defined nucleotide sequences given in the  
 CC specification. The polypeptide is useful in the manufacture of a  
 CC medicament for treating a syndrome associated with a human disease. The  
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
 CC further used as hybridisation probes, in chromosome mapping, tissue  
 CC typing, preventive medicine, and pharmacogenomics. The present sequence  
 CC encodes a NOVX polypeptide of the invention.

Sequence 8010 BP; 1720 A; 2411 C; 2141 G; 1738 T; 0 U; 0 Other;

Query Match 75.1%; Score 7616.4; DB 12; Length 8010;  
 Best Local Similarity 97.8%; Pred. No. 0;  
 Matches 7824; Conservative 0; Mismatches 1; Indels 177; Gaps 3;

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QY 1 ATGGGCGGGGCGCCCTCCCGCTTGTGCTGCTGCTTGTGATCTGAGCTGCTGT 60
DB 1 ATGGCGGGGCGCCCTCCCGCTTGTGCTGCTGCTGCTGCTGATCTGAGCTGCTGT 60
QY 61 GCTAGCAATCAGGAGACTCCGTGGGCGTAGAGACCTCCGAGCTAGTCAAGAACTT 120
DB 61 GCTAGCAATCAGGAGACTCCGTGGGCGTAGAGACCTCCGAGCTAGTCAAGAACTT 120
QY 121 GAGTTAAAGTCTGAGGTGTAAGTGTATGCCAGCAAAAGACAGCAAGAGCTGT 180
DB 121 GAGTTAAAGTCTGAGGTGTAAGTGTATGCCAGCAAAAGACAGCAAGAGCTGT 180
QY 181 GGTTAATCAGGTGTGTGTGTCCAGAGCAATAATGTGTCCAACTGTGCAATGCC 240
DB 181 GGTTAATCAGGTGTGTGTGTGTCCAGAGCAATAATGTGTGTCCAACTGTGCAATGCC 240
QY 241 GAAAGGGGCAAAAGACTAGGCTCGATTTTCAAGTTAGATCCAGCTCCAGTTCACTCG 300
DB 241 GAAAGGGGCAAAAGACTAGGCTCGATTTTCAAGTTAGATCCAGCTCCAGTTCACTCG 300
QY 301 AACGAGGCTATGACTGCAAGGGTCCAAAGCGGATCACTGTATGAAAGTACGACATG 360
DB 301 AACGAGGCTATGACTGCAAGGGTCCAAAGCGGATCACTGTATGAAAGTACGACATG 360
QY 361 TTTGGGCGCTGGAGGAGCAAGGCGAGTGTGCGGAGCCCGCATGTGTATGCCACTT 420
DB 361 TTTGGGCGCTGGAGGAGCAAGGCGAGTGTGCGGAGCCCGCATGTGTATGCCACTT 420
QY 421 CGAGGCGCCCTCGGAGCATCATCACTCCCAATTTTCCCATTCAGATGACAAATGCA 480
DB 421 CGAGGCGCCCTCGGAGCATCATCACTCCCAATTTTCCCATTCAGATGACAAATGCA 480
QY 481 CACTGTGTGTGATCATCAAGACTCAACCCCTCCAAAGTGTATCAAGCTCGCTTTGAG 540
DB 481 CACTGTGTGTGATCATCAAGACTCAACCCCTCCAAAGTGTATCAAGCTCGCTTTGAG 540
QY 541 GAGTTGATTTTGGAGGGGCTATGACACCTGACCGGTGATGTGTGTGTGTGTGAG 600
DB 541 GAGTTGATTTTGGAGGGGCTATGACACCTGACCGGTGATGTGTGTGTGTGTGAG 600
QY 601 GACGAGAAAGAGATTCTCTCAATGTCTCAAAATGCTGCAAGTACAGCCCTCAACCCCA 660
DB 601 GACGAGAAAGAGATTCTCTCAATGTCTCAAAATGCTGCAAGTACAGCCCTCAACCCCA 660
QY 661 GCGTCTCGCATCCCAAGAGCAATGTCTGGGAGCATCTGAGAGGAGAAATGAGACTGTACT 720
DB 661 GCGTCTCGCATCCCAAGAGCAATGTCTGGGAGCATCTGAGAGGAGAAATGAGACTGTACT 720
QY 721 GAGATGTGTGTGACATTTAGAGCTTCAATGTCTCAAAATGCTGCAAGTACAGCCCTCAACCCCA 780
DB 721 GAGATGTGTGTGACATTTAGAGCTTCAATGTCTCAAAATGCTGCAAGTACAGCCCTCAACCCCA 780
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DB 841 GGTGACCTCTGGCATTAATCTGATATGAGCCGAGAGGAAAGCTCCCGGTTTACACCGGTGAC 900
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DB 1741 TACCAAGGAGCCCAAGTTTCCAGTTTCCATCAGACAGAGAACTACTTCACTCTCCCTC 1800
QY 1801 TTCTCTACCGAACAAGTCACTCGGACATGTGCTTCCAGCTTCCGCTATGAGACTATTA 1860
DB 1801 TTCTCTACCGAACAAGTCACTCGGACATGTGCTTCCAGCTTCCGCTATGAGACTATTA 1860
QY 1861 CTGCACTGAGACCACTGTCTGTGATCAGAGAAATCCAGTAAATGAGACAGCTCATGGAAAT 1920
DB 1861 CTGCACTGAGACCACTGTCTGTGATCAGAGAAATCCAGTAAATGAGACAGCTCATGGAAAT 1920

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QY 1921 GACTTCTAGTGGGGCCGCTGTGTGACTTCACTGTGTGACTCGGCTACACATTAAGTAC 1980  
Db 1921 GACTTCTAGTGGGGCCGCTGTGTGACTTCACTGTGTGACTCGGCTACACATTAAGTAC 1980  
QY 1981 GGGGAGCCTCTGTGAGTGTGAGCCCAACTTCCAGTGAAGCCGGGACCTCCAGTTGTGA 2040  
Db 1981 GGGGAGCCTCTGTGAGTGTGAGCCCAACTTCCAGTGTGAGCCGGGACCTCCAGTTGTGA 2040  
QY 2041 GCTCTGTGTGTGCTTCACTTCAAGGCTTCAGTGGGACCATTTGTCCGACAGGTTCCCT 2100  
Db 2041 GCTCTGTGTGTGCTTCACTTCAAGGCTTCAGTGGGACCATTTGTCCGACAGGTTCCCT 2100  
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QY 3901 AGCAATGTGGCTGTGATTAATGATTAAGAAAAACCGCGGAGTCAATGTTTGAATCT 3960  
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QY 4021 TACTACTGCAAGGAGGCTAGAGAGTGAAGGCACTTGAACCTGAGCTGATCTGGGG 4080  
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XX 22-AUG-2002.  
 XX 10-DEC-2001; 2001MO-US048369.  
 XX 08-DEC-2000; 2000US-0254329P.  
 PR 14-DEC-2000; 2000US-0255648P.  
 PR 15-MAY-2001; 2001US-0291037P.  
 PR 08-JUN-2001; 2001US-0292173P.  
 PR 08-JUN-2001; 2001US-0309258P.  
 PR 29-AUG-2001; 2001US-0315639P.  
 PR 01-OCT-2001; 2001US-0326393P.  
 XX (CURA-) CURAGEN CORP.  
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 PI Colman SD, Edinger SR, Ellerman K, Gerlach V, Gorman U, Grosse WM,  
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 PI Millet I, Pena CE, Peyman JA, Raselli L, Rieger DK, Shinkels RA,  
 PI Smitheon G, Szytek KA, Stone DJ, Tchernev VT, Vernet CM, Voss EZ,  
 PI Zernhusen BD, Zhong H, Zhong M;  
 DR WPI; 2002-643486/69.  
 DR P-PSDB; ABG79169.  
 XX  
 PT New NOVX polypeptides and polynucleotides useful for treating or  
 PT preventing e.g. neurodegenerative diseases, neurological disorders,  
 PT cardiovascular diseases, muscular diseases and disorders, or  
 PT immunological diseases.  
 XX  
 XX Claim 9; Page 14-16; 299pp; English.  
 XX  
 CC The present invention relates to new NOVX polypeptides. The polypeptides,  
 CC polynucleotides and antibodies are useful in the manufacture of a  
 CC medicament for treating or preventing neurodegenerative diseases (e.g.  
 CC Alzheimer's disease, Parkinson's disease, or Huntington's disease),  
 CC neurological disorders (e.g. anxiety, schizophrenia, manic depression or  
 CC mental retardation), cardiovascular disease (e.g. acute heart failure,  
 CC angina pectoris or myocardial infarction), muscular diseases and  
 CC disorders, retinal diseases (including those involving photoreception,  
 CC deafness and keratinisation disorders), cancer (e.g. ovarian cancer or  
 CC melanoma), immunological disorders, inflammatory and immune diseases,  
 CC bacterial, fungal, protozoal and viral infections, and reproductive  
 CC system disorders. The proteins of the invention may be used to screen  
 CC drugs or compounds that modulate the NOVX protein activity or expression,  
 CC as well as to treat disorders characterised by insufficient or excessive  
 CC production of NOVX protein or protein forms that have decreased or  
 CC aberrant activity compared to NOVX wild type protein, such as diabetes,  
 CC obesity, metabolic disturbances associated with obesity, anorexia and  
 CC wasting disorders associated with chronic diseases and various cancers,  
 CC infectious diseases and various dyslipidaemias. The nucleic acid  
 CC sequences of the invention may be used in chromosome mapping, identifying  
 CC an individual from minute biological samples (tissue typing), and in  
 CC forensic identification of a biological sample. The present nucleic acid  
 CC sequence encodes a NOVX protein of the invention  
 XX  
 XX Sequence 8010 BP; 1720 A; 2412 C; 2140 G; 1738 T; 0 U; 0 Other;  
 SQ  
 Query Match 75.1%; Score 7614.8; DB 6; Length 8010;  
 Best Local Similarity 97.8%; Pred. No. 0;  
 Matches 7893; Conservative 0; Mismatches 2; Indels 177; Gaps 3;

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 DB 241 GAAAGGGGCAAAAAGACTAGGCTCGATTTTCAGTTAGATTCAGGCTCCAGTTCACTGCG 300  
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 DB 481 CACTGTGTGTGATCATCAAGACATCAACCCCTCCAGGTGATCAAGCTCGCTTTGAG 540  
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Qy 4081 CCTGATGGGAAGCCCGTGTGAAACAATCCCGGACAGTCTGACAGCCCTTGTGGGGAG 4140  
Db 4081 CCTGATGGGAAGCCCGTGTGTGAACAATCCCGGACAGTCTGACAGCCCTTGTGGGGAG 4140  
Qy 4141 CAGTATGTGGGTTCCGACGAGAGTGTCTTGTCCCAACTACCCCGAAGCTACACAGT 4200  
Db 4141 CAGTATGTGGGTTCCGACGAGAGTGTCTTGTCCCAACTACCCCGAAGCTACACAGT 4200  
Qy 4201 GGAACATCTGCTTGTATTTTGTACTGTCTCCCAAGACTATGTGTGTGGCCAGTTTC 4260  
Db 4201 GGAACATCTGCTTGTATTTTGTACTGTCTCCCAAGACTATGTGTGTGGCCAGTTTC 4260  
Qy 4261 GCTTCTTTCAACGCGCCCTCAACGAGTGTGAGAGTTTCAAGCGGCAACAGCCAGCAC 4320  
Db 4261 GCTTCTTTCAACGCGCCCTCAACGAGTGTGAGAGTTTCAAGCGGCAACAGCCAGCAC 4320  
Qy 4321 TGGCGGCTCTCAGCTCCCTCTGCGGCTCCCATACAGAGAACTACTGCTTGTGGCCACC 4380  
Db 4321 TGGCGGCTCTCAGCTCCCTCTGCGGCTCCCATACAGAGAACTACTGCTTGTGGCCACC 4380  
Qy 4381 TCCATCAAGTTTCTATTAAGTTCAAGGCCAAGGCTTGTGACAGCCAGAGGCTTTCAC 4440  
Db 4381 TCCATCAAGTTTCTATTAAGTTCAAGGCCAAGGCTTGTGACAGCCAGAGGCTTTCAC 4440  
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Db 4441 TTTGTCTACCAAGCGGTTCTTGAACGAGGCAACGAGTGAAGCTGTGTCGGGAATCC 4500  
Qy 4501 CGGTATGGCAAGAGCTGGGCAATGACTTCTCGGTGGGGCCATCGTCCGCTTCCGAATGC 4560  
Db 4501 CGGTATGGCAAGAGCTGGGCAATGACTTCTCGGTGGGGCCATCGTCCGCTTCCGAATGC 4560

Qy 4561 AACTCCGCTATGCTCCCTGACGGGGTCCGACAGATCGAGTGTCTCCCTGTGGGGCC 4620  
Db 4561 AACTCCGCTATGCTCCCTGACGGGGTCCGACAGATCGAGTGTCTCCCTGTGGGGCC 4620  
Qy 4621 TTGGCCCAATGGAATGTCTCAGCGCCACGTGTGTGTGTCGGTGAAGCAACTTACA 4680  
Db 4621 TTGGCCCAATGGAATGTCTCAGCGCCACGTGTGTGTGTCGGTGAAGCAACTTACA 4680  
Qy 4681 GAGCGAGGGGACCACTCTGTCTCCCTGGCTTCCAGAGCCGTACTCAACAGCTTCAAC 4740  
Db 4681 GAGCGAGGGGACCACTCTGTCTCCCTGGCTTCCAGAGCCGTACTCAACAGCTTCAAC 4740  
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Db 4741 TGTGTGTGAAGATGTGTGTGTCGCCGAGAGGCGCTGGATCCAGTGTGCACTTTT 4800  
Qy 4801 GTGACAGACAGAACTGGGACTCTGCTGGAAGATTTGATGTGTGACATTAACATGTATAC 4860  
Db 4801 GTGACAGACAGAACTGGGACTCTGCTGGAAGATTTGATGTGTGACATTAACATGTATAC 4860  
Qy 4861 ATGCTGGGAGTTTCTCAGGAAACACGCTGCTGCTTCTGAAACAGCACTTCCAAACAG 4920  
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Db 4921 CTCTACTCTCATTTCTACTCAGATATCAGGATATGACGCTGCTTCACTTGGAGTAC 4980  
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Db 5581 TGAATGACCTTGAAGCTTCCCGGGATTCATTTGACTGGCAACCTGTCTCAGTGT 5640

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DB 5701 GGGAACTACCTTCTTCCAAAGGCACTGTGTACTCCCGGGGTTCCCTGAGCCCGTACTCC 5760  
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DB 5761 AGCTCCAGGACTGTGTCTGGGTGATCAACCGTCCCATTTGGCCATGGCGTCCGCTCAAC 5820  
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DB 5941 TCATCCAAACAGAGTCTGCTCAAGTTCACCGTGTAGCAGCCAGGGGGGATCTTGGC 6000  
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QY 6421 CTGAAGGCTCAGTGGGAATTACTCAGTCCCTGATGTCACAGCTCAAGCAACTCT 6480  
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DB 6721 CCTCTGTCAAGCTCTTCTCTGTGGGCTTCTGTAGGCCCCCAAGATGGAATGTGTGT 6780  
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DB 6901 GTCCCAACCAAGTGTCTC-----CTGTGACTGTCTCT 6933  
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QY 7561 GTGC----- 7624  
DB 7561 GTGC----- 7624  
QY 7624 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7680  
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DB 7801 CCACTGCAAGATCATCACTGTGACAGATCTGTGACACCAAGAAATAGTGTGTGAG 7863



Db	1025	CAGGAAATGCAAGATCAAGCTGTGTGAAGATCGAAGACAGATTCTTTGGAGCCAGC	1084
QY	3589	CCGGCAACATCATGCTCTCCCTCGGGGGAGACTCGACAGACCATCTGAGTCATCTC	3648
Db	1085	CCGGCAACATCATGCTCTCCCTCGGGGGAGAAGCTCGACAGACCATCTGAGTCATCTC	1144
QY	3649	TCACCAATTACCCGAAACCTTACCCCGCAGGCAAGAGTGTGACTGGAAAGTACCGTC	3708
Db	1145	TCACCAATTACCCGAAACCTTACCCCGCAGGCAAGAGTGTGACTGGAAAGTACCGTC	1204
QY	3709	TCACCAAGCTACGTCATGCGCCCTGGTATTTAACATCTTTAACCTGGAAGCTGCGTATAC	3768
Db	1205	TCACCAAGCTACGTCATGCGCCCTGGTATTTAACATCTTTAACCTGGAAGCTGCGTATAC	1264
QY	3769	TTCTCTCATATCTACGACGAGCAGGAGCTCTCTCAGCCCTCTCATAGAACTTCTATGAC	3828
Db	1265	TTCTCTCATATCTACGACGAGCAGGAGCTCTCTCAGCCCTCTCATAGAACTTCTATGAC	1324
QY	3829	TCCCAAGCTCCCAAGCGCCGATTTGAAAGCAGCAACACCTCTTCTGCTTCCGACAGC	3888
Db	1325	TCCCAAGCTCCCAAGCGCCGATTTGAAAGCAGCAACACCTCTTCTGCTTCCGACAGC	1384
QY	3889	GATGATCTGTGAGCAATGCTGAGCTTCGTCACTTACGCTTACGAAAGAACCCCGGGAGTCA	3948
Db	1385	GATGATCTGTGAGCAATGCTGAGCTTCGTCACTTACGCTTACGAAAGAACCCCGGGAGTCA	1444
QY	3949	TGTTTTGATCCTGGTTCATCAAGACGGCACACGGGTGGGGTCCGACTTGAAGCTGGGC	4008
Db	1445	TGTTTTGATCCTGGTTCATCAAGACGGCACACGGGTGGGGTCCGACTTGAAGCTGGGC	1504
QY	4009	TCTCTCCGACACTACTACTGACACGGGGGGCTTACGAAAGTTGAGGGACCTGCACCTGAGC	4068
Db	1505	TCTCTCCGACACTACTACTGACACGGGGGGCTTACGAAAGTTGAGGGACCTGCACCTGAGC	1564
QY	4069	TGCATCTCTGGGGCCTGATGAGAGGCCCGTGTGGAACAATCCCGGCCAGTCTGCACAGCC	4128
Db	1565	TGCATCTCTGGGGCCTGATGAGAGGCCCGTGTGGAACAATCCCGGCCAGTCTGCACAGCC	1624
QY	4129	CCCTGTGGGGGACAGTATGTGGGTTCCGACGGAAGTGTCTTGTCCCCCACTACCCCGAG	4188
Db	1625	CCCTGTGGGGGACAGTATGTGGGTTCCGACGGAAGTGTCTTGTCCCCCACTACCCCGAG	1684
QY	4189	AACCTACACAGTGGACAGATCGCTGTATTTTGTATCTGTGCCCCAAGACTATGTGTG	4248
Db	1685	AACCTACACAGTGGACAGATCGCTGTATTTTGTATCTGTGCCCCAAGACTATGTGTG	1744
QY	4249	TTTGGCCAGTTGCGCTTCTTTACACGGGCCCTCAACGACGTGTGAGAGTTTACGACGGC	4308
Db	1745	TTTGGCCAGTTGCGCTTCTTTACACGGGCCCTCAACGACGTGTGAGAGTTTACGACGGC	1804
QY	4309	CACAGCCAGCACTCGCGGCTCTCAGCTCCCTTCGGGCTCCCAAT	4354
Db	1805	CACAGCCAGCACTCGCGGCTCTCAGCTCCCTTCGGGCTCCCAAT	1864
QY	4355	-----	4354
Db	1865	TCGGCAATGTGGGAATGTGTGGGCCGGGGGCACTACGTCGGCTAAAGAAAGAGGC	1924
QY	4355	-----	4354
Db	1925	TCTAGAACACCCCATGCGCGGAGTGAACCTTACGGCTCTGCGTGCCTGTGHTTCT	1984
QY	4355	-----	4354
Db	2045	AGCTGCCCTCACCCGAGACTGTGTACACACCGCCCTTGTGTGTGAGCTTCTCTGTG	2104
QY	4355	-----	4354

Db	2105	AATGGCAACTAACAATAATTGGCTGCAAGSTGCAGTGGTGCTGTCTCCCTGGCCATC	216
OY	4355	-----	4354
Db	2165	TGTACTGCACCAAGCAAGAAATATACCTTGTCTTGCTACAAGAAAGCTGACTACC	2224
OY	4355	-----CAGAGAAATCACTGCGCTTGGGCACCTCCAAATCAAGTCTC	4395
Db	2225	CTGGTTTCTGTGTGCCATGCAAGAGAAATCACTGCGCTTGGGCACCTCCAAATCAAGTCTC	2284
OY	4396	ATTAAAGTTTACGCGCAAGGCGCTTGACACCAAGCAGAGGCTTTCACATTGTCTACA----	4451
Db	2285	ATTAAAGTTTCAAGCGCAAGGCGCTTGACACCAAGCAGAGGCTTTCACATTGTCTACAAGGT	2344
OY	4452	-----AGCGGTTCTTGAAACAGCGCCACGCAAGTGCAGCTGTGTG	4491
Db	2345	ATGAGAGCAATGACGCGCGAGCGGTTCTTGAAACAGCGCCACGCAAGTGCAGCTGTGTG	2404
OY	4492	CCGGAACCCCGCTATGCGAAGAGGCTTGGGCAATGACTTTCTCGGTGGGGGCTATGTCGCG	4551
Db	2405	CCGGAACCCCGCTATGCGAAGAGGCTTGGGCAATGACTTTCTCGGTGGGGGCTATGTCGCG	2464
OY	4552	TTGCAATGCAACTCCGGCTATGCGCTGACAGGGGTGGCGACAGATCGAGTGCCTCCGTGTG	4611
Db	2465	TTGCAATGCAACTCCGGCTATGCGCTGACAGGGGTGGCGACAGATCGAGTGCCTCCGTGTG	2524
OY	4612	CCTGGGGGCTTGGGCCAATGGAATGTCACGCGCCACGTGTGTGTGTCGCTGTGAGGC	4671
Db	2525	CCTGGGGGCTTGGGCCAATGGAATGTCACGCGCCACGTGTGTGTGTCGCTGTGAGGC	2584
OY	4672	AACTTCACAGAGCGCAGGGGCAACATCTCTGCTCCCTTGGCTTCCAGAGCCGTACTCAAC	4731
Db	2585	AACTTCACAGAGCGCAGGGGCAACATCTCTGCTCCCTTGGCTTCCAGAGCCGTACTCAAC	2644
OY	4732	AGCCTCAACTGTGTGTAAGATGTGTGTCCCGAAGGCGCTGGCAATCCAGATCAAGTT	4791
Db	2645	AGCCTCAACTGTGTGTAAGATGTGTGTCCCGAAGGCGCTGGCAATCCAGATCAAGTT	2704
OY	4792	GTCAGTTTGTGACAGAGCAGAACTGGGACTCGCTGAGATATTGATGTGTGACATTAAC	4851
Db	2705	GTCAGTTTGTGACAGAGCAGAACTGGGACTCGCTGAGATATTGATGTGTGACATTAAC	2764
OY	4852	ACTGTAAACATGCTGGGGAAGTTTCTCAGAAACAACCGTGCTGCTTCTGAAACGACAC	4911
Db	2765	ACTGTAAACATGCTGGGGAAGTTTCTCAGAAACAACCGTGCTGCTTCTGAAACGACAC	2824
OY	4912	TTCACAACAGCTACCTTCAATTTCTACTCAGATATCAGCGTATCTGACGCGGCTTCCAC	4971
Db	2825	TTCACAACAGCTACCTTCAATTTCTACTCAGATATCAGCGTATCTGACGCGGCTTCCAC	2884
OY	4972	TTGGAGTACAAAAACGATGGGCGCTGAGCAGTTGTCCGAAACCTGTGTGCCAGTTAACGGG	5031
Db	2885	TTGGAGTACAAAAACGATGGGCGCTGAGCAGTTGTGTCCGAAACCTGTGTGCCAGTTAACGGG	2944
OY	5032	GTTGAAGACTGGCGAGCGCTACTTGTGATGATGTGTGTCTTCCAGTGTAGCCGGGA	5091
Db	2945	GTTGAAGACTGGCGAGCGCTACTTGTGATGATGTGTGTCTTCCAGTGTAGCCGGGA	3004
OY	5092	TATGCGCTTCCAGGGGCAACGCCCAATCTCTCTGCAATGCCCGGAACAATGGCCGCAATGAAAC	5151
Db	3005	TATGCGCTTCCAGGGGCAACGCCCAATCTCTCTGCAATGCCCGGAACAATGGCCGCAATGAAAC	3064
OY	5152	TACCTCCTCACTCTGTATTTGACAGATGTGGGGGAACAATGAGAGAGATGAGAGGGGTG	5211
Db	3065	TACCTCCTCACTCTGTATTTGACAGATGTGGGGGAACAATGAGAGAGATGAGAGGGGTG	3124
OY	5212	ATCTGTAGCCCGGCTTCCAGGCAACTAACCCAGTAACATGACTGTCTCTGTGAAATA	5271
Db	3125	ATCTGTAGCCCGGCTTCCAGGCAACTAACCCAGTAACATGACTGTCTCTGTGAAATA	3184
OY	5272	GCACTGCCCGTGGGCTTTGAGACTCAATCAAGTTCTTGAATCTTCCACACGAGCCCAAC	5331
Db	3185	GCACTGCCCGTGGGCTTTGAGACTCAATCAAGTTCTTGAATCTTCCACACGAGCCCAAC	3244



QY 5332 CACGATACATAGAAATCCGGAAATGGCCCTATGAGCCAGCCGATGAGGAAATTC 5391  
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Db 3245 CACGATACATAGAAATCCGGAAATGGCCCTATGAGCCAGCCGATGAGGAAATTC 3304  
| | | | |  
QY 5392 AGTGAAGCGAGCTTCCAGAGCTCCCTCTCCAGCTCCCGAGACACCGGTATATTC 5451  
| | | | |  
Db 3305 AGTGAAGCGAGCTTCCAGAGCTCCCTCTCCAGCTCCCGAGACACCGGTATATTC 3364  
| | | | |  
QY 5452 CACAGGACCACTCCCAAGATTCGGCCAGATTCAGCTGAGATCAG----- 5499  
| | | | |  
Db 3365 CACAGGACCACTCCCAAGATTCGGCCAGATTCAGCTGAGATCAG----- 3424  
| | | | |  
QY 5500 ----- 5499  
| | | | |  
Db 3425 TCCCAACCAATTTCTTCTTCTGAGAGGTTTGATCTCGAGATTGGAAGAACCAAC 3484  
| | | | |  
QY 5500 -----GCTTAT 5505  
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Db 3485 TCMACTCTCCGCTCGCCGCTCTCTATGTCGGGATCTTGATCTGTTGTGAAGCTAT 3544  
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QY 5506 GAACCTTCAAGAGTGGCCAGACCCAGAGCCCTTTGGCAATGGCATTTGTAGGGAGCTGGC 5565  
| | | | |  
Db 3545 GAACCTTCAAGAGTGGCCAGACCCAGAGCCCTTTGGCAATGGCATTTGTAGGGAGCTGGC 3604  
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QY 5566 TACAAGTGGGACCAATCAAGTACCTTCAGTGGCTCCGGGGATGATCAATTTGATGGCAC 5625  
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Db 3605 TACAAGTGGGACCAATCAAGTACCTTCAGTGGCTCCGGGGATGATCAATTTGATGGCAC 3664  
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Db 3665 CCTGTCCTCAAGCTGCAATGACCAACCGGAACTGGGACCAACCCCTGCCCCAGATGT 3724  
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| | | | |  
Db 3725 GAAGTCCCTTGTGGGGGAAATCATCTTTCCAAAGGCACTGTGATCTCCCGGGGTTTC 3784  
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QY 5746 CCTAGCCGTAATCCAGCTCCGAGAGCTGTGTGCTGATGATCAACGGTGGCC---ATTGGC 5802  
| | | | |  
Db 3785 CCTAGCCGTAATCCAGCTCCGAGAGCTGTGTGCTGATGATCAACGGTGGCC---ATTGGC 3844  
| | | | |  
QY 5803 CATGGCGTCCGCTCAACCTCAAGCTGTGTGACAGAGAGCCCTGTGGAATTTTCATACC 5862  
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Db 3845 ATGGGGGTCCGCTCAACCTCAAGCTGTGTGACAGAGAGCCCTGTGGAATTTTCATACC 3904  
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QY 5863 ATCTGGGATGGGCAACAGCAACAGCAACAGGCTGGGGCTTTCAACCCGAGACATGGCC 5922  
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QY 5923 AAGAAAACAGTGAGAGTTTCATCAACAGGTCCTGCTCAAGTTCCACCGTATGAGGC 5982  
| | | | |  
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| | | | |  
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| | | | |  
Db 4085 ACCATCTTCCCAACCCCGAAGTGTGTACAGAGATGAAGATTCAATATAGGTGATC 4144  
| | | | |  
QY 6103 GTACGCTAGAGATGCTCCCTGCTTACCTTATGTTGGGAGTGAATTTCTGACCTGCA 6162  
| | | | |  
Db 4145 GTACGCTAGAGATGCTCCCTGCTTACCTTATGTTGGGAGTGAATTTCTGACCTGCA 4204  
| | | | |  
QY 6163 CTGGAACCTACCTGAGATTGAAGACACACCCCGATATGTGAATGAGACTGTCCACA 6222  
| | | | |  
Db 4205 CTGGAACCTACCTGAGATTGAAGACACACCCCGATATGTGAATGAGACTGTCCACA 4264  
| | | | |  
QY 6223 AATGAGCTTCTGACAGATTCACAGGCGTGTATCTTGAAGCAGACTTACCTGGAAGCTAT 6282  
| | | | |  
Db 4265 AATGAGCTTCTGACAGATTCACAGGCGTGTATCTTGAAGCAGACTTACCTGGAAGCTAT 4324  
| | | | |

QY 6283 CCCAGATTCCAGACCTGCTCTTGGCTGTGAGAGTGGAGCCGCAATATAATCTCCCTC 6342  
| | | | |  
Db 4325 CCCAGATTCCAGACCTGCTCTTGGCTGTGAGAGTGGAGCCGCAATATAATCTCCCTC 4384  
| | | | |  
QY 6343 ACAGTGAATCTTCTCTCAGCAGAGAAAGCAATATGATGATTTTGTATGATTTTGA 6402  
| | | | |  
Db 4385 ACAGTGAATCTTCTCTCAGCAGAGAAAGCAATATGATGATTTTGTATGATTTTGA 4444  
| | | | |  
QY 6403 TCAGGACAGAGTCTCTGTGAAAGCCCTCAGTGGGAATTTACTAGCTCCCGATTTTC 6462  
| | | | |  
Db 4445 TCAGGACAGAGTCTCTGTGAAAGCCCTCAGTGGGAATTTACTAGCTCCCGATTTTC 4504  
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QY 6463 ACCAGCTCAAGCAACTGTGTATCTGCTGGTGTATCTGATCAACGCTCAATGGAAG 6522  
| | | | |  
Db 4505 ACCAGCTCAAGCAACTGTGTATCTGCTGGTGTATCTGATCAACGCTCAATGGAAG 4564  
| | | | |  
QY 6523 GGCTTCAAGATCCGCTATTCAGCCCTTCACTGACGCTGCCAGGGCTCACTCATGAGC 6582  
| | | | |  
Db 4565 GGCTTCAAGATCCGCTATTCAGCCCTTCACTGACGCTGCCAGGGCTCACTCATGAGC 4584  
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QY 6583 TTCTATCTAGGCAACGACACCCAGCCCGGGGGCTCCATCCATTTGGTCCAGCC 6642  
| | | | |  
Db 4585 -----AGGCCAGACGACACCCAGCCCGGGGGCTCCATCCATTTGGTCCAGCC 4636  
| | | | |  
QY 6643 GGCTACCGCTGATGGGACACAGACATGGGCACTGTATCCCGGCAACCCCGAGGCTACAC 6702  
| | | | |  
Db 4637 GGCTACCGCTGATGGGACACAGACATGGGCACTGTATCCCGGCAACCCCGAGGCTACAC 4696  
| | | | |  
QY 6703 CTGTGGAGGAAAGCAATCCCTCTGTGTCAAGCTCTTTCTGTGGGCTTCTGAGGCC 6762  
| | | | |  
Db 4697 CTGTGGAGGAAAGCAATCCCTCTGTGTCAAGCTCTTTCTGTGGGCTTCTGAGGCC 4756  
| | | | |  
QY 6763 AAGATGGAATGATGTTTGGGAAAGATCAACATGAGGAAACCAAGGCGGTATCAGTGC 6822  
| | | | |  
Db 4757 AAGATGGAATGATGTTTGGGAAAGATCAACATGAGGAAACCAAGGCGGTATCAGTGC 4816  
| | | | |  
QY 6823 AAGTGAAGCTACCACTCCAGGACGAGGCTGAGGACCACTGACAGAGTGTCTGACACAGC 6882  
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| | | | |  
QY 6883 CTATGAGGCAACCGCAATGTCCACCAAGTGTTC----- 6919  
| | | | |  
Db 4877 CTATGAGGCAACCGCAATGTCCACCAAGTGTTC----- 4936  
| | | | |  
QY 6920 ----CTGTATCTTGTCTGATGTCAATGATCAAGTGTGAGAGTGTGAGAGCTT 6975  
| | | | |  
Db 4937 GGATCTGTGATCTTGTCTGATGTCAATGATCAAGTGTGAGAGTGTGAGAGCTT 4996  
| | | | |  
QY 6976 ATCTTTGAGACAGATATGATTCAGGCGCAGCTGATGCTCATCTGTGACCTGTGCTAC 7035  
| | | | |  
Db 4997 ATCTTTGAGACAGATATGATTCAGGCGCAGCTGATGCTCATCTGTGACCTGTGCTAC 5056  
| | | | |  
QY 7036 TACTATCTGACCAAGGATTCATCCGCTGTGAGGCAATGGAATGAGAGCTCGGGAGC 7095  
| | | | |  
Db 5057 TACTATCTGACCAAGGATTCATCCGCTGTGAGGCAATGGAATGAGAGCTCGGGAGC 5116  
| | | | |  
QY 7096 TCTAGGCCCACTGCGCAATCATCTCTGTGAGAGTCTCCGATTTCCCGCAATGGCCAC 7155  
| | | | |  
Db 5117 TCTAGGCCCACTGCGCAATCATCTCTGTGAGAGTCTCCGATTTCCCGCAATGGCCAC 5176  
| | | | |  
QY 7156 CGCATGGAACACTGTCTGTCTACAGGGGCAACAGGCATTTCTCCGCAATTCGGGATAC 7215  
| | | | |  
Db 5177 CGCATGGAACACTGTCTGTCTACAGGGGCAACAGGCATTTCTCCGCAATTCGGGATAC 5236  
| | | | |  
QY 7216 ACACTGTGGGCTCAGGGTGGTGAAGTGCATGAGCCATGGGCTCTGAGTGGCTTGA 7275  
| | | | |  
Db 5237 ACACTGTGGGCTCAGGGTGGTGAAGTGCATGAGCCATGGGCTCTGAGTGGCTTGA 5296  
| | | | |  
QY 7276 GTCCGCTGCTT----- 7287  
| | | | |  
Db 5297 GTCCGCTGCTT-----GCTGACACTGTGGGACTCTGAGCCCATTTGTC 5356  
| | | | |  
QY 7288 -----GCTGACACTGTGGGACTCTGAGCCCATTTGTC 7320  
| | | | |

[illegible]

Pd		07-FEB-2002.
XX		
PF		24-JUL-2001; 2001WO-US023322.
XX		
PR		02-AUG-2000; 2000US-0222504P.
PR		28-NOV-2000; 2000US-00728787.
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Weicher AA, Elliott GS;	
XX		
DR	WPI; 2002-303934/34.	
PP	-P-PDB; AAE20788.	
PT		
XX		
PS	Claim 1; Fig 3; 251pp; English.	
CC		
CC	The invention relates to a nucleic acid encoding a novel C3b/C4b	
CC	complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like	
CC	polypeptide and nucleic acid molecules may be used to treat, prevent,	
CC	ameliorate, diagnose and/or detect diseases such as immune system	
CC	disorders such as rheumatoid arthritis, psoriatic arthritis, autoimmune	
CC	arthritis, osteoarthritis, inflammatory joint disease, autoimmune	
CC	diseases, multiple sclerosis, lupus, inflammatory bowel disease,	
CC	transplant rejection, nervous system disorders (e.g. Alzheimer's	
CC	disease), ischemic conditions, metabolic disorders (e.g. obesity and	
CC	diabetes) and infertility. The invention is useful in gene therapy. The	
CC	present sequence is rat C3b/C4b complement receptor like cDNA	
XX		
SQ	Sequence 12525 BP; 3136 A; 3208 C; 3002 G; 3106 T; 0 U; 73 Other;	
	Query Match	41.3%; Score 4183.2; DB 6; Length 12525;
	Best Local Similarity	66.3%; Pred. No. 0;
	Matches 6076; Conservative	1; Mismatches 3065; Indels 25; Gaps 3;
OY	819 AGAGATGAGCAGCGGCATTGGCGGTGACCTTGCAATCTGCATATGTCAGCGGAGGAAG	878
Db	153 AGAATCATGAGAAGGAGGCTCGGGGACCTTGCATCCAGCCTAACGGAAACGGACTGG	212
OY	879 CTCCCGGTTTCACCAGCGGTGACACACTCAAGTTTAGTGCAGGCCGCTTTGAGTGT	938
Db	213 CAGCAGCTTTTGGACGGGGACAGCTCACCTTTGAGTGCAGGACAAGCTTTTGAAGTGGT	272
OY	939 GGACACAGAAGCATCATGCCCCAAAGAAATAACCAATGTCGCGCTTAAGAACCAAGCTG	998
Db	273 AGGAGAGAGATGATTAAGTGCAGGAACAAACACAGTGTGTCGGCAACAGCAAGCTG	332
OY	999 CGTGTTCCTCGCTTTCTTCAAATTCACACAGCCGCTGSGGGTTTCTGTCTCCCACTA	1058
Db	333 TGTTTTTCATGTTTCTTCAAATTCACAGGCGCTCTTGGATCATCTGTGCCAAACTA	392
OY	1059 CCAGAGACTATGSCAACCACTTCCAATGTGTGCTCATCTTGCCAGGCTTGAGAG	1118
Db	393 TCCTGAGGAATATGSCAAACATGAAATGTGTGTGTTATATCTGAGCCCCGGAG	452
OY	1119 CCGCATCACTGCGCTTTCACAGCATTTGAGAGTGAAGCTTCAAGTTTGAATTTCCGTGAT	1178
Db	453 CCGAATTCACCTCATCTTCAATGATTTTCAGATGGAAGCTTCAAGTTTCACTTGGCGT	512
OY	1179 CAAGAGTGGGCGCACCGCGAGGGGCGCCGCTCTGGGACCTTTCAGAGAAACAGCTTCC	1238
Db	513 CAAGAGTATGATGGATTTCTTGACATCAACAGTCTCTGGGACTTTCTCTGGCAATGAGTGC	572
OY	1239 CTCCTCATCAACAAGAGTGGCCAGTGGCCGCTCTCGAGTTTCCAGACTGACCTCAC	1298
Db	573 TGCACAGCTGGCCAGCAGTGGACACATAGTACGCTGGAATTTCAAGTCCATCACTTAC	632
OY	1299 AGGAAAGAGGGGCTTCAACATCACTTTTACCACTTCGACACAAACGATGCCGATCC	1358

Db 633 CACGGGACAGGGGTTCAACATCATATATACACACATTTGGTTCAGAAAGATGATGATGCC 692  
 Qy 1359 TGGCGTTCCAGTAAATGGGAAAGGTTTGGGACACCTCCAGCTGGGAGCTCCATCTC 1418  
 Db 693 TGGGATCCCTGTGAATGGACGGGCTTTGGAGACAGATTTCTGGGGAAGTTCTGTGTC 752  
 Qy 1419 CTTCCTCTGTGATGAGGCTTCCCTTGGGACTCAGGGCTCAGAGACCATCAGCTGCTCT 1478  
 Db 753 CTTCCTCTGTGATGAGGCTTCTGTGAAAGTCTCAGGGTCTGAGTCTATCAGATGATCTT 812  
 Qy 1479 GAAGAGGGCAGCGGTGTGTGAACAGCGCTGTGCTGCGGTGGAAGCTCCCTGTGTG 1538  
 Db 813 GCAGATGGAAGAGTGGTCTGAGAGCTCTACTGCTCCGCTGTGAAGCTCTGTGTGTG 872  
 Qy 1539 TCACCTGATTTGGCCAGCGGACCATCTCTCTCCGGCTGGCTTGGCTTCTACAGGA 1598  
 Db 873 GCATCTGACAGCTTCTAGTGGGGTCAATATTACTTCAGAGTGGCCAGGATATTAACAAA 932  
 Qy 1599 TGGCTTGAAGCTGCTGGGTGATGAGGGCCAGCGGCTACCCCATCAAAATCAGCTT 1658  
 Db 933 TTTCTTAAATTGGGAATGGGTCAATTGAAGCCAAACAGACATTCATCAAAATTAACATT 992  
 Qy 1659 CGACAGATTCAAAACGAGGTCAACTATGACACCTGGAAGTACGCGATGGGCGAGCTTA 1718  
 Db 993 TGAAGATTCCAGACAGAAAGTCAATTATGATCTTGAAAGTCCGGGATGGGCAACAG 1052  
 Qy 1719 CTGAGGGCTTGTATGGGGTTTACACGAGAACCGAGTTCCCACTTCTCTATCAGCAC 1778  
 Db 1053 CTCATCCCACTGATGGGAGTACATGACACCGAGCTCCACAGTCTCTATCAGCAC 1112  
 Qy 1779 CAGCACTACCTTACCT 1838  
 Db 1113 AGGGAATCATATCTACTGCTGTTTACACTGACAGACCGGCTGAGTGTGGCTTCT 1172  
 Qy 1839 GCTCCGCTATGAGACTATTAACCTGAGTCAACCTGATGATCCAGATCCAGT 1898  
 Db 1173 CATCTCATGAGAGTGTACTTGTATCTGATCTGATCTGATCCGGGCAATCCCTGT 1232  
 Qy 1899 AATGAGACAGCTGATGGGAATGATCTTACGTGGGCGCTGTGTACTTCACTGTGTGA 1958  
 Db 1233 AATGATCATCGGACAGGAGTAACTTTGGTATCAATCTACAGTACCTTCACTGTGTGA 1292  
 Qy 1959 CTCGGGCTACACTTAAGTGAAGGGGAGCTCTGAGTGAAGCCCACTTCCAGTGGAG 2018  
 Db 1293 CCTGGGTACACCTCAGATGATACATCCCTCATCTGTGAGAAAGAACATCAGTGGAA 1352  
 Qy 2019 CCGGGCCCTGCGCAGTTGTGAAGCTCTGTGTGGCTTCAATCAAGGCTCCAGTGGAG 2078  
 Db 1353 CCAAGCTTGGCCAGCTGTGATGCCCTGTGTGAGGCTACATCCATGGAAAGAGTGGAC 1412  
 Qy 2079 CATCTGTGCGCAGGGTCCCTGATCTTCAACCCCAACACTGAACTGACCTGATTAAT 2138  
 Db 1413 TGTCTTTTCAACAGGATTTCCAGACTTTTATCCAACTCTGAACTGATCAGTGAACAT 1472  
 Qy 2139 CGAAACATCTCAGGAGGAGGTGTCTTCACTTTTCCACACTTCCACCTGGAAAGTGG 2198  
 Db 1473 TGAAGTCTCTCAGGAGGAGGTGAGATGAATTTCCACACTTTCACCTTAAAGTTC 1532  
 Qy 2199 CCACTGACTACCTCTCTCATCTAGAGAACGAGACTTCAACGAGCCCTGTGAGAGCTAAC 2258  
 Db 1533 CCAAGACTATTTGCTGATCAAGAGAGTGGAGTTTCTCAGAGCCGTTAGCCAGCTCAC 1592  
 Qy 2259 TGGATCTCGGCTGCGAGCTCCATCAGCGCTGGGCTTATGGCACTTCACTGCGCAAGT 2318  
 Db 1593 TGGGTGGTCTGCTGCTCACAACATTAAGGCTGGCTGTGTGGAAACTTCACTGCGCAACT 1652  
 Qy 2319 CCGCTTCTATCTGATTTTCTCAGTATGATGAAAGTAAAGATCAATCACTTCTCAGAGTA 2378  
 Db 1653 CAGATTCATCTGACTTCTCAGTCTCTCTATGAAAGGCTTCAACATTAAGTTTCAAGATA 1712  
 Qy 2379 CAGACTTGAAGCCCTGTGAGAGCGAGGCTCCAGGCTTACAGCATCCGGAAGGAGCTTGA 2438  
 Db 1713 TGAACTAGAACCTGTGATGATCCTGTGAAGTCCCTGCTTACAGTCCGAGAAATTTGGTTCCA 1772

Qy 2439 GTTTGGCGGGGAGACACCTTGAACCTTCTCTGCTTCCCGGGTACCGTCTGAGAGGCAC 2498  
 Db 1773 GTTCGATGTGGGTGACACCTTGGCTTTCACTGCTTCCAGGATACCGCTTGAAGGTGC 1832  
 Qy 2499 CGCCGCACTCAGTGTCTGGGGGAGACAGCGGCTGTGAGTCTGCTTCCAGAGTG 2558  
 Db 1833 AACCAAGCTTACCTGCTGGGTGGGGAGCGGAGTGTGAGTGAACCTTCTCCAAAGTG 1892  
 Qy 2559 TGTGTGATGTGGGAATTCAGTCAAGGACCTCAGGTAATTTGTGTGTCCCAACT 2618  
 Db 1893 TGTGTGATGTGGAGCAAGGCTCAAGGAATGAAGGAATTAATCTTCTCAAAATT 1952  
 Qy 2619 TCCCTGAACTCAATTAACATCATGAATGATCTACTCATCCAGACCCAGGAGAA 2678  
 Db 1953 CCCATTCATTTATGATTAATACATGATGTATCTATTAATTAAGAAACGAAGCCGGA 2012  
 Qy 2679 GGGAAATTCAGTGAAGCCAGGAGCATTTGCACTTCCGAAGGAGATGTCCTCAAGTTTA 2738  
 Db 2013 GGGGATTCATCTCAGAGCCGGAACCTTCCACTTTCGAAGGAGACACTTAAAGTTTA 2072  
 Qy 2739 TGAATGCAACAACTCCGCGCTTGTGTGAGATTTTACCATTTGAGATGATGG 2798  
 Db 2073 TGAATGAAAGACAGCTCTCTGAGGTCACTGGAAGTCTTCAAGAAAGTGAATGAG 2132  
 Qy 2799 GGTGACTTTGAACAGACATCCAGCAGTGTGTGATTTTCACTGATGCTGA 2858  
 Db 2133 GCTGTGCTTAACAGACTTCCACACCTGAGGCTGAGGTTCACTTACAGGGTCA 2192  
 Qy 2859 CACAGCAAGGCTTGAACCTGACATTTTCAAGTTTGAATCATCAATGAAGAGACC 2918  
 Db 2193 TACCGCCAAAGCTTCAAGCTCACTCACTCAAGTTTGAATGAATGAAGATCC 2252  
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 Db 2253 AGGCAATCCCTTAATGTGTGTAAGATGATGATGATGATGATGATGATGATGATGAT 2312  
 Qy 2979 GTTCCTTCACTGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATG 3038  
 Db 2313 TCTTCAAGCTGACACAGGCTTCCAGATGATGATGATGATGATGATGATGATGATGAT 2372  
 Qy 3039 TGAAGAGCCGAGACCTGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3098  
 Db 2373 TGGGAGCCGAAGGTGTGGGACAAACCTATGCTTCTGTGTGGGGAATGTGTGTCT 2432  
 Qy 3099 AGTGAAGAGAGGTGTGGGGAGGTGTGATCCCGGATATCAAGTCTCTATGAACA 3158  
 Db 2433 CGTCAATGACGACATCAGAGAGCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2492  
 Qy 3159 CAATCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3218  
 Db 2493 CAACCTTCAATGACTTGAACATGAGGCTGATCTTGGCAAGACCAATCAAGCTTCAAT 2552  
 Qy 3219 CTTGTGTGTGAACAGAGAGGTTTCAACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 3278  
 Db 2553 CATGTGTGTGAACAGAGAGGTTTCAACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2612  
 Qy 3279 GAGCGGGGTTTGTGTAAGAGCTGATGATGATGATGATGATGATGATGATGATGAT 3338  
 Db 2613 CAGCAATCTCTGCTGAAGAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2672  
 Qy 3339 CTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3398  
 Db 2673 CTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2732  
 Qy 3399 CATTAATTTTCAAGTGTGACAGCAAGCTCTGCAATGATGATGATGATGATGATGAT 3458  
 Db 2733 CATCAAGTCTCTCACTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 2792  
 Qy 3459 GAGTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3518  
 Db 2793 AACCCGTAATGTGACAGCGGGGAACCTGGAAGACATACACTTCAAGTGTGATCCTGG 2852

QY 3519 CTACGGCTGACAGGAGTGCAGAGATCAGTGTGTGAAGATCGAAGACAGGTTCTTCTG 3578  
DB 2853 ATATCCAGCTTCCAGGGCAAGCCAGATCACTTGTGTGAGCTTAAACAACCGCTTCTTCTG 2912  
QY 3579 GCAAGCCAGCCCGCAACATGCATCGCTCCCTGCGGGGAGACCTGACAGAACATCTGG 3638  
DB 2913 GCACACGAGCCCTCCCTCATGTACATGCTGTGTGGGAAATCTGACAGGCCCTGCTGG 2972  
QY 3639 AGTCATCCTCTACCAAAATTAACCAACCTAACCCCGCAGGACAGAGATGTGACTGGA 3698  
DB 2973 AGTGAATTTTATATCCCAACTTACCCACAGCATACCTCTCGGAGAGAGATGTGACTGGAG 3032  
QY 3699 AGTGAACCTGTCAACAGACTAGCTCATCGCCCTGTGATTTAAATCTTTAACTGTGAGCC 3758  
DB 3033 AATTAAGTGAACCCGACTTTGTGATGTGCTTAAATTTCAAAAGTTTAAAGATGAGCC 3092  
QY 3759 TGGCTATGACTTCTTCATATCTACAGAGAGGAGCTTCTGAGCCCTCTCATAGGAAG 3818  
DB 3093 AAGTAAAGACTTCTGACATATCTATGAAAGGAGCTCAACAGCCACTGATCGGAAG 3152  
QY 3819 CTTCATAGGCTCCAGCTCCAGCCGCAATGAAAGCAGACAGAGCTTCTCTGCG 3878  
DB 3153 CTTCAGAGGTTCTCAAGCCCAAGAGATGAGAGAGTGTAAAGCTTCTCTGCG 3212  
QY 3879 CTTCGACAGATGATCTGTGAGCAATGCTGCTTCTCATTTGAATATACAGAAACCC 3938  
DB 3213 ATTCAGAGATGATGCTCTGTGGCTGTCCGGGTTGCAATTTGAATTTAAAGAAACC 3272  
QY 3939 GCGGAGTATGTTTGTATCTGTGTTCCATCAAGAACGAGCAACGCGGTGGGCTCCGACT 3998  
DB 3273 AGGGAGAGCTTCTTGAACCTGAGGAAATATGAAAGGAGCAAGATTTGAAACGAGACT 3332  
QY 3999 GAAGTGGGCTCTCCGCTACCTACTACGCAAGGAGGCTACGAAATGAGGAGCACTC 4058  
DB 3333 TAAAGTGGGCTTCAAGTTACTATCAATGTGACTGTGTAAAGATTTGTGATCTTC 3392  
QY 4059 GACCTGAGCTGATCTGTGGGCTGTATGAGAAAGCCGCTGTGAAATATCCCGGCACT 4118  
DB 3393 ATTCATGAGTGTGTGACAGGGAGCTGATGGAAAGCCGCTGTGGAACCGGCACTGCG 3452  
QY 4119 CTGACAGGCCCCCTGTGGGGGAGATGTGTGGTTGGAACGAGATGTCTTGTCCCA 4178  
DB 3453 CTGCAAGAGACCTGTGGAGGCAATATACATGGCTCTGAGAGGGGTATGTTGTCAACAA 3512  
QY 4179 CTACCCCCGAGACTACACAGAGTGCAGATCTGTTGTTATTTGTTAATGTCGCAAGA 4238  
DB 3513 CTACCTCTATCTACAGGCTGTGGGAGATGATCTATTTCTATCAACGATGCCAAGGA 3572  
QY 4239 CTATGTGTGTGGGCAAGTTGCTTTTCAACGCGCTCAACGAGTGTGTGAGGT 4298  
DB 3573 ATTTGTGTGTGTGACAGTTGTGCTATTTTCAAGCTGGGCTGAACGACTTGGCAAAAT 3632  
QY 4299 TACAGACGCGCAACAGCAGACTGCGGCTCTGAGCTCCCTGTGGGCTCCCATACAG 4358  
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QY 4359 AGAATCACTGACCTTGGCACTCCCAATCAAGTTCTCATTAAGTTCAAGGCCAAAGGCT 4418  
DB 3693 TGAACACCTCCGCTGCTACATCTCAATCAATGATTTGCTTGGCTTCAAGCGCAAAAGCGG 3752  
QY 4419 GCGACAGCAGAGGCTTCACTTTGTCTACCAAGCGGTTCTCTGACAGCGCCAGCA 4478  
DB 3753 AGCTTCTGACAGGGGTTTCCACTTGTCTACCAACCGCTCCACCAAGTGAACGCA 3812  
QY 4479 GTGAGCTCTGTGCGGGAACCCGCTATGTGCAAGAGGCTGGGAGTGAATTTGCGTGGG 4538  
DB 3813 GTGAGCTCTGTGCGGGAACCGCTATGTGCAAGAGGATGTGATTTCTGACAGG 3872  
QY 4539 GGGCATCTGCTGCTTGAATGCAATCGGCTATGCTCCGCAAGGCTGCGAGAGATGA 4598  
DB 3873 CTCCATCTGCTGCTTGAATGCAATCGGCTATGCTCCGCAAGGCTGCAACGCAATCG 3932  
QY 4599 GTGCTCTGCTGCTGCTGAGGCTTGGCCCAATGAAATGTCTCAAGCCCAAGTGTGTGT 4658

DB 3933 TTGTGAGTGTGTGCCAAACGCTTTGGCCCAAGTGAATACACATCCCAAGTGTGTGT 3992  
QY 4659 GCGGTGTGAGGCAACTTCAAGAGCGAGCGACCATCTGTCTCTGCTTCCAGA 4718  
DB 3993 TCCATGAGTGTGCAATTTCACTCAGAGAAAGGGCAATCTTATCTCCAGGCTACCTGA 4052  
QY 4719 GCGGTACTCAACAGGCTCAACGTGTGTGGAAGAATGTGTCTCCGGAAGCGGTGGAT 4778  
DB 4053 GCGCTTATGGAACAACTGAATGTGTATGGAAGTCAATGATGTGAGGGCTCAGGGAT 4112  
QY 4779 CCAGATCCAAAGTGTCACTTTGTGACAGACAGAACTGGGACTGCTGAAGTATTTGA 4838  
DB 4113 COAGATCAAGTATTTACTTTGCAACGAGACAGAACTGGGACTCCGAGATCATAGA 4172  
QY 4839 TGTGTGAGATTAACATGTAAACATGTGTGGGAGTTCTCAGAAACACGCTGCTCCT 4898  
DB 4173 CGAGGAGACATGACGCGCCCAAGCTGGGCAAGCTTCTCAGATACACAGTGCAGCACT 4232  
QY 4899 TGTGAACAGCACTTCAACAGCTCTACCTTCAATTTCTACATACAGATATGCTGCG 4958  
DB 4233 GCTGATATGCACTTCAACAGCTCTGTGCACTTCCAGTGGACATGATGTGCGCG 4292  
QY 4959 AGCTGGCTTCCACTTGAAGTCAAAACGCTGGGCTGAGCAGTTGTCCGAACTGTGT 5018  
DB 4293 TCGCGGCTTTCACCTGGAATCAAAACGCTGGTCTGGCTGCGTGCAGGAACCTGCTCT 4352  
QY 5019 GCCCATTAACGGGCTGAAGATCTGCGAGCGCTACTTGTGATATGATGTGTCTTTCA 5078  
DB 4353 CCCAGCAACGGGCAATCAAGATGAGAACCGCTATATGTGTGAACATGTGTCTTCCA 4412  
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QY 5139 GCGGAGATGAATCACTCCTCTCCACTGTATTTGCAACATGTGTGGGGAACATGAGGA 5198  
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QY 5199 GATGAGAGGGGTATCTGTAGAGCCCGGCTTCCAGGCAATCAACCAATGATGATG 5258  
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QY 5259 CTCCGTGAATAATPACACATGCGCGGTGTGGAGCTCACTCAGTCTTGAATCTGCTC 5318  
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QY 5319 CACGAGCCCAACAGCACTACATAGAAATCGGAATGCGCTTATGAGACAGCGCAT 5378  
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QY 5379 GATGGAAGATTTCAATGTGGAAGCGAGCTTCCAGAGCTCTCTCTCCAGTGTCCAGAGAC 5438  
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DB 4773 CCTATCTGCTTCTATATGTACCACTCAGAAACCGAACAGATTTTAACTCACTTACCA 4832  
QY 5499 GGCCTATGAACCTTCAAGAGTGCAGACCCAGAGCCCTTTGCAATGTGAGAGG 5558  
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DB 4893 CTTCGATTTACAGCTGTGGCCAGTGTGATCTATTTGAGTGTCTACCCGGGCTACATCTTGT 4952  
QY 5619 TGGCAACCTGTCTCTCAAGTGTCAATGGAACCAACGGAATCTGGAGCAACCCCTGCGC 5678  
DB 4953 AGGCAACCTGTGTCTCAAGTGTGCAAGTGTGCACTGAGAACTGTGAACCTTCTTCC 5012  
QY 5679 CAATGTGAAGTCTCTGTGGCGGGAACATCACTTCTTCAACGGAACGTGTACTCCC 5738

Db 5013 ACGGTGACGCTCCCTGTGGTATATGATCATCAGAAATGSCACATTATTTCCCC 5072  
Qy 5739 GGGGTCCCTAGCCCTACTCCAGCTCCAGGACTGTGTCTGCTGATACCTGTGCCAT 5798  
Db 5073 TGGGTCCAGAGAGATTCATCAATTCGAAAGACTCTGTGTGTGTCACTGTCTCC 5132  
Qy 5799 TGGCATGGCGTCCGCTCAACCTCAGCCCTGTCAGACAGAGCCCTCTGAGATTTCAT 5858  
Db 5133 AGGACATGGAGTGTATCATCACTTCACCTTGTCTGACAGCTGAGAGCTGTAAATGACTACAT 5192  
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Db 5193 CGCTGTGGAGTGTCTGTGACAGAACTGTCTGAGCTGTGGGCTCTTCACTGGAACAC 5252  
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Db 5253 TGGCTTCGAGACAGCATACAGCTCCACCAACAGGCTTGTCTCAATTCACAGCATTT 5312  
Qy 5979 AGCCACAGGGGGGATCTTGCCTAGCTTTCTCGCTTATCCACTACCAAAATGCCCTGC 6038  
Db 5313 CTCCAATGGAGCTTCTTGTCTCTCAATTTTCATGCAATTTCACTGAAGAGTGCCTGC 5372  
Qy 6039 TCCACCATCTCCCAAGCCGAGTGTGTACAGAGAAATGAATTAATAGTGA 6098  
Db 5373 TCTCCAGTAGTCCGACAGCTGACTGCTTACAGAAAGATGAAGACTTTGAATAGGGA 5432  
Qy 6099 CATGTACGCTACAGATGCTCTCCCTGTCTTACCTTATGTGGGAATGAATTTGACCTG 6158  
Db 5433 CTTCGTAAGTACCAAGTGCATCAGGGTACAGCTGTGGGAAGTGAACCTCTGACATG 5492  
Qy 6159 CAACTTGGAACTTACCTGAGTTTGAAGAACCCCGATATGTAAGTGCAGTGTGC 6218  
Db 5493 CAACTCAGCTCAGCTATTTTCCAAAGCTTCCACCTACCTGTGAAGACATATGCC 5552  
Qy 6219 AACAAATGAGCTTCTGACAGACTCAAGAGCTGATCTGAGCCAGAGCTACCTCGAAG 6278  
Db 5553 AGCCAAATGAAGTGCAGAGAGTCTTCTGGGTGATTTCTCACTCGGGATACCAAGCA 5612  
Qy 6279 CTTATCCCACTTCAAGCTGTCTGTGTGTGAGAGTGAAGCCGACTATTAATCTTC 6338  
Db 5613 CTAATTTAACTCCCAACATGTGCTGTGAGTATTAAGTGAAGCCAACTTTAACTTAC 5672  
Qy 6339 CCTCAGATGGAGTACTCTCTCAGCGAAGCAATATGATGATTTGAATTTTATGAG 6398  
Db 5673 GCTCTTTGTGAGACCTTTTCAAGTAAAGCAATTTGATGACTGGAAGTATTTATGAG 5732  
Qy 6399 TCCATCAGGACAGAGTCTCTGTGTAAGCCCTCAGTGGGAATTAATCAGCTCCCTGAT 6458  
Db 5733 TTTCTTGGGCAAAAGTCTTTGTAGTGTCTTAAGTGGGAACCACTGAACAGTCCAA 5792  
Qy 6459 TGTCACTAGCTCAAGCACTGTGTACTGTGTGTGTCTGATCAAGCTTCAATCG 6518  
Db 5793 TTTTACAGAGAAATACCATCTGTACTCCGCTGTCCACAGATCATGCAACAGCA 5852  
Qy 6519 GAAAGGCTTCAAAATCCGCTATTCAGCCCTTACTGACAGCTGCCAGAGGCTCCACTCCA 6578  
Db 5853 GAAAGATTTCAAAATTCGTATGCTATGCTCTTACTGAGCTTCACTTCACTCAAGAA 5912  
Qy 6579 TGGCTTCACTCTAGGCGACAGACCCAGCCCGGGGCTCATCTCACTTTGGCTGCA 6638  
Db 5913 TGGTGGCGTTTAAATAAACCGCAGCGCCCTGGGGAAGCAAGTGTGAGATTTCTGCA 5972  
Qy 6639 CGCGGCTTACCGCTGTGTGGACACAGATGCTCATCTGTATCCCGCAACCCCAAGGCTTA 6698  
Db 5973 GCTGTGATATCGATATGTCAGACAGCAACGCACTGCAAGCGGAACCAATGTGGCGCT 6032  
Qy 6699 CCACTGTGAGAGGAAGCAATCCCTCTGTCTCAAGCTCTTCTGTGTGGCTCTCAAGGC 6758  
Db 6033 GTACAGTGGAGTTCATGAGCAACGCTTGTGCAAGGCTGTCTGTGAAATTCACAGGC 6092  
Qy 6759 CCCCAAGAAATGATGATGTGTGTGCAAGAGTACAGAGTGAAGCAAGGCGCTGTACAG 6818  
Db 6093 TCCAGGAATGCTGTCTGCTTCAAGGCAATGAGTTCACTTATGAGATGAAGTGACTTATGA 6152

Qy 6819 CTGACATGAAGGCTACCACTTCAGGACAGCGCTGAGGCCACTGACAGATGTCTGAGCAC 6878  
Db 6153 ATGTATATGAAGCTTCAAGCTGATGATGCCAGTACAGAACCACTGCTGTGTGCAAGAA 6212  
Qy 6879 AGCCCTATGAGCAACCGCAATGTCCACACAGTGTGTCTGTGACTTGTCTGATGT 6938  
Db 6213 TGGCTGTGAGCAACAGAGAAAGCACCCAGTGAACCCGAGTGTGCCCTGCCCCAGCAT 6272  
Qy 6939 CAGTACATCAGCGTGAAGCATGCGCGATGAGAGCTTATCTTTGAGACAGATATCAGT 6998  
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Qy 6999 CAGGCGCCAGTATGCTCATGTGTGACCTGGCTACTACTATACCTGACCAAGGTCAT 7058  
Db 6333 TGAAGTCAAGTCTCTCAGCTGTATGCTGTGACTTCTTGTGAGAGTCAAGGCTGT 6392  
Qy 7059 CCGCTGTACAGCCAAATGGCAATGAGAGCTCGGGAATCTACGCCACCTGCGAATCAT 7118  
Db 6393 GCAAGTCCAAAGCCAAATGGGACTTGAACACTGAGAGGACAGACCCAGATGTAAAGTCA 6452  
Qy 7119 CTCTGTGAGAGCTCCGATTTCCGCCAATGGCCACCGCATGGAACACTGTCTGTCTA 7178  
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Qy 7179 CGGGCAACAGCATCTTCTCTGCAATTCGGGATACACAGTGTGGGCTCCAGGGTGG 7238  
Db 6513 TGAAGCAACCGCATCTTCACTGTCAATACCGGCTACACATTTGATGGCTCCATGTCCG 6572  
Qy 7239 TGAAGTATGACCAATGGGCTGTGAGTGTCTGAAAGTCCGCTGCTGTGACACTG 7298  
Db 6573 GGAAGTCTTGGCAATGTCTGTGAGGAGTCTGAACAAAGTGTCTGGGGTCAATGG 6632  
Qy 7299 TGAAGTCTTGAAGCCCATTTGTCAAGACATCAATGGGGAATCACTACCTACCGGG 7358  
Db 6633 TGGCTCTCAGAGCCCATTTGTGAATGCGCATATCAGTGGCTGATCAGCTTACAGGGA 6692  
Qy 7359 CAGTGTGTGTACCAATGATAGCTGTGGCTCCGCTGATCCGATGTCTGTGCGCATCG 7418  
Db 6693 CACAGTGTCTACCAATGACCTGTGGTGTGTGACTGTGAGCAAGTGTGAGAGTTTG 6752  
Qy 7419 CCAGAGATCATCACTGTGCGGCAAGACCCCTTCTGTGTGTGCAATTAATTCCTGTGACA 7478  
Db 6753 CTTGACAGACCAACAGTGTGTGGGCAAGACCCCGTTGTGCTCCCATACATGTGAGACA 6812  
Qy 7479 CCAAGCAACCTGTCAACAGGCTTCACTGAGGTAACAGTTTAACTTCAACAGATGTGT 7538  
Db 6813 CCTGGAACCTGTCCATGTGCTCAACCAAGGAGCGATTCAACTGAATGACCTTGT 6872  
Qy 7539 CAAATTTGTTCGAACCTGTGGTATATGCTGAGAGGGGTGTAGTCCCAATGCTGTGC 7598  
Db 6873 GAATTTTCACTGTCCATACGGGCTTACTGTGAGGAGTGTCTCCAGGCCAAATGTGGAG 6932  
Qy 7599 CAGCGGCAATGGAATGACATGCTGCCACTGCAAGAAATCATCACTGACATGATCTGTG 7658  
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Qy 7659 AACACGAATAATGATTTGTGTCAGGTCCACGACCGGCGGCAACAGGTTCACTTGG 7718  
Db 6993 ATTTGTGAAATATGAGTTTCCGACAGGCAACAGAACTTTCCAGAGAGTTTGAATGAG 7052  
Qy 7719 CACCACTGTGTCTTACCGGTGCAACAGGCTTCTTACCTCTGTGGGCAACCCAGTGTGAG 7778  
Db 7053 GACAAATGTGATGTATCACTGTCAAAAGAGGTTTCACTTGTGGCTCTTGTGCCCTGAC 7112  
Qy 7779 CTGCAAGGAGATGAGCAATGGAACGTCCTCCGCGCCCAAGTGTCTTGTGTCTCTGTGG 7838  
Db 7113 CTGCAATGCAAGTGTGTGTGGAACCGCTCTTACCAAGTGTCTGTGCTATATCATGTGG 7172  
Qy 7839 CCAATCGGGCTCCCGCTCACTCCCAATGTCTGTGAAGCAATTAATCTGTGAGAGCACT 7898  
Db 7173 GCATCTGTGGGTCCCGCTAATGTGTCTGTGAGTGAATAATTTTAACTTTGAGGCCAC 7232

QY 7899 GGTGGGATACAGCTCATCGGACGATCTGTGGGAAAACAGACCCGAGTGTGG 7958  
 DB 7233 AGTTAGTACTCTCGAAGGGGGCCAGATTCTCAAGGCATATGACAAAGGTCTGCA 7292  
 QY 7959 GCTGATGAGACATGAGCTGCTCCCTCCCTCACTGCTCAGAACCCAGCGTGGAGTTTG 8018  
 DB 7233 AGAACAAGTCACTGAGAGTGAATCCCTTCCCATTTGTTCAAGAAAATAGCTCGAGATTTTGG 7352  
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 DB 7353 TGGTATTCAGGAGACCCAGCAAGTGGGTCTGTCTTGGGAGTGAATTMAACAAGAG 7412  
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 DB 7413 TCTTTTGGGATTTCTCTGTGAGATGGGCCACAGCTGGGGGTTCTGACAGACGACATG 7472  
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 DB 7473 CTTGATGATGGGTCTGTGATCAGAGATCCAGCTGTGTGTGAGGCGGTCTGTGAAA 7532  
 QY 8139 CCTGGGATCCAGATGATGCCGAGTTGTTCAGTGA TGGCTGTGTTTTCTCAGCTC 8258  
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 QY 8319 GGTCAATGATCCTTGGACAGGCAATGACCTTGAAGTCTCTGTATMAACTGTGTGACCC 8378  
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 DB 7773 CTATCAGTGCACCTCGGCTACCTGATGAGGCCCAACATCACCAACATCCGCTGAC 7832  
 QY 8499 CAGAGCCGACATGAGATGAAACCAAGCCGCTGTGCAAAAGCTCTCATGTGCAAGCAC 8558  
 DB 7833 CAATAATGATCATGGAATCAGACCCGCGCTCTGCAAAAGCTGTCTATGACAGCAGC 7892  
 QY 8559 TCCGCTATCCCAATGGGAGTGGTGGGCTGATCATGTGGGGTCAAGTGTGAC 8618  
 DB 7893 TCCCTCAGTGCACAAAGGAGTGGAGGCTGACATTCGATGGGGTCCAGCATAG 7952  
 QY 8619 TTATGCTGCTGAGAGGATACAGCTCTCCTGCGCGGATGTTCACTGTGAGGAAA 8678  
 DB 7953 CTACAGTTGTGTGATGCTACAGCTCCCATCTGGCCATCTGTCTGTGAAAGGGG 8012  
 QY 8679 TGGGTCTGAGACCGAGAGCTGCTCATGTTCCTGTGTTCTGCGGGGATCTGTGTGT 8738  
 DB 8013 TGGAGTATGGAAGGAGAGTCCCTCAGTGTGCTGTGTCTGTGGGATCCAGGAC 8072  
 QY 8739 CCGGTCCGCTGGAGAGAGAGACCGAGCTTCCTCTACAGTATCTGTCTCTTCTC 8798  
 DB 8073 TCCAGCAGAGGACGGCTCAGTGGGAAAGCTTACCTTTAAGTCTGAGGTTTATCA 8132  
 QY 8799 CTGCAATCCCTCTGTGTGCTGTGGGCTCTCAGCAGAGTTTTCAGTCAATGAGAC 8858  
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 QY 8859 ATGAGTGGACCCAGCCCACTGATGATCGAAGCTGACACGTTGTGGGACCTGTGG 8918  
 DB 8193 GTGGAGTGGCATCAGCCCACTGTATAGATCAGGCCACACGGTGTGCCAGACCCGG 8252  
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DB 8313 CTTCAATGTAGAAAGGTTTACCATCTCAAGGCTCCACTCCGAGCTGTCTTCCAA 8372  
 QY 9039 CCGTACCTGAGTGAAGAACCCCACTGACTGTGTCCCAACACATCGAGGCGAGAC 9098  
 DB 8373 CCGTACCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 8432  
 QY 9099 GCCAAGCATGCAAGCTCGGGGCTGTGATTTCCCTCATGAGGCTTACAGCTCAT-TA 9157  
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 DB 8493 CACTGTGATCAGAGATTTTCTTGTGCGGATGTGAGCAGACGTTGAAAGCAGA 8552  
 QY 9218 TGGCAGCTGAGCAGGCAAGCCGCTCATCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 9277  
 DB 8553 CATGAATGACAGAGAAAGTCACTGTT-----GTAAAGTAAAG 8594  
 QY 9278 CAACACTGCGCGGAGCCACCGCTCACCAAGCTTGAATCTGAGGATGTTTTGCGCA 9337  
 DB 8595 AGTGAAGAAATTAATGAACAGTTACTMAAATCCAGTCTCTGTATGATTTTTCAT 8654  
 QY 9338 GAATTCCTGTGAAAGGCGCTATGAAATACAGGAGAAAGAGAGCCAGCTGTGAG 9397  
 DB 8655 CACTCGGTGTGAAAGGATATTAATGAAATATTAGGCAAGAGACAGCCGCGACTCTAC 8714  
 QY 9398 AGTACTGTGCTTCCAAAGTTCGCAACAGCAAGTCAATGCAATGATGACACAGTGG 9457  
 DB 8715 TGTGATCTGTTTAATGAAACAGCAGCAAGTCAATGCACTTCAAGGCTTCA 8774  
 QY 9458 CGTGAAGCTGCACTTGTGAGAACTTCAAGAAAGAAATTTTATCTCTACTCTCAAGT 9517  
 DB 8775 GTGCAAGTGAAGCTGACAGGAGCTTACAGAAAGAAAGGCGCACTGTCTGAAAGC 8834  
 QY 9518 GTACCAATTAACAGGCGCTGTGAGATCTTGAATTAATGATTAAGTCAAGTGTGAG 9577  
 DB 8835 CTTTCATATCAAGGCGCAGAGATTTTGTGAAGCAAGTTTAAATGACACTGAGG 8894  
 QY 9578 TTTAGATGAGGATGCTGCTGAGAGTCTCTCGGAGCCACTTCAATACCAAGCTGT 9637  
 DB 8895 ACTGATGATTAATATCTGAGACTTGAAGCTTGAAGAGAGAGATCTCTTCAAGGATAT 8954  
 QY 9638 CAAGGCGCAAGCTTGTGAGAGTGTGAGCTTCAAGACTGAGCTGTGAGTGTGAG 9697  
 DB 8955 ACATGAAAGAACTTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 9008  
 QY 9698 AGACCCGAGTCAATGAGCGCACTTGTCTTCAACAGAGCTGAGTGTGAGAGTGTGAG 9757  
 DB 9009 TGATGAGATTTCTCAATCATATACAGGAGCAGCAGAGTGTGAGAGTGTGAGAGTGTGAG 9068  
 QY 9758 CCGTGTGCTTCAATGAGCTTCAATGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 9817  
 DB 9069 TCTGTGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 9128  
 QY 9818 GAGAAGACCAAGTCTTCAATGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 9877  
 DB 9129 AACAAAGCAAAAGTTCATATGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 9188  
 QY 9938 GCGGAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 9984  
 DB 9249 GTTGAACAGCTGTGAGACAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 9295

RESULT 13  
 ADH72215  
 ID ADH72215 standard; DNA; 10989 BP.  
 XX  
 AC ADH72215;



XX 25-MAR-2004 (first entry)  
 DT Human gene of the invention NOV54b SEQ ID NO:1111.  
 XX  
 DE  
 XX ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;  
 XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;  
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
 KW obesity; diabetes; infectious disease; metabolic syndrome X;  
 KW dyslipidaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2003102155-A2.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PF 03-JUN-2003; 2003WO-US017430.  
 XX  
 PR 03-JUN-2002; 2002US-0385120P.  
 PR 04-JUN-2002; 2002US-0385784P.  
 PR 05-JUN-2002; 2002US-0386041P.  
 PR 06-JUN-2002; 2002US-0386047P.  
 PR 06-JUN-2002; 2002US-0386376P.  
 PR 06-JUN-2002; 2002US-0386453P.  
 PR 06-JUN-2002; 2002US-0386864P.  
 PR 06-JUN-2002; 2002US-0387016P.  
 PR 07-JUN-2002; 2002US-0386796P.  
 PR 07-JUN-2002; 2002US-0386816P.  
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 PR 07-JUN-2002; 2002US-0386942P.  
 PR 07-JUN-2002; 2002US-0386971P.  
 PR 07-JUN-2002; 2002US-0387262P.  
 PR 08-JUN-2002; 2002US-0296960P.  
 PR 10-JUN-2002; 2002US-0387400P.  
 PR 10-JUN-2002; 2002US-0387535P.  
 PR 11-JUN-2002; 2002US-0387610P.  
 PR 11-JUN-2002; 2002US-0387625P.  
 PR 11-JUN-2002; 2002US-0387634P.  
 PR 11-JUN-2002; 2002US-0387688P.  
 PR 11-JUN-2002; 2002US-0387696P.  
 PR 11-JUN-2002; 2002US-0387702P.  
 PR 11-JUN-2002; 2002US-0387836P.  
 PR 11-JUN-2002; 2002US-0387859P.  
 PR 12-JUN-2002; 2002US-0387933P.  
 PR 12-JUN-2002; 2002US-0387934P.  
 PR 12-JUN-2002; 2002US-0387960P.  
 PR 12-JUN-2002; 2002US-0388022P.  
 PR 12-JUN-2002; 2002US-0388066P.  
 PR 13-JUN-2002; 2002US-0389123P.  
 PR 14-JUN-2002; 2002US-0389118P.  
 PR 14-JUN-2002; 2002US-0389120P.  
 PR 14-JUN-2002; 2002US-0389144P.  
 PR 14-JUN-2002; 2002US-0389146P.  
 PR 17-JUN-2002; 2002US-0389729P.  
 PR 17-JUN-2002; 2002US-0389742P.  
 PR 18-JUN-2002; 2002US-0389884P.  
 PR 19-JUN-2002; 2002US-0390066P.  
 PR 19-JUN-2002; 2002US-0390209P.  
 PR 21-JUN-2002; 2002US-0390763P.  
 PR 17-JUL-2002; 2002US-0396706P.  
 PR 06-AUG-2002; 2002US-0401628P.  
 PR 09-AUG-2002; 2002US-0402156P.  
 PR 09-AUG-2002; 2002US-0402256P.  
 PR 09-AUG-2002; 2002US-0402389P.  
 PR 12-AUG-2002; 2002US-0402786P.  
 PR 12-AUG-2002; 2002US-0402816P.  
 PR 12-AUG-2002; 2002US-0402821P.  
 PR 12-AUG-2002; 2002US-0402832P.  
 PR 13-AUG-2002; 2002US-0403448P.  
 PR 13-AUG-2002; 2002US-0403459P.  
 PR 13-AUG-2002; 2002US-0403531P.  
 PR 13-AUG-2002; 2002US-0403532P.

PR 13-AUG-2002; 2002US-0403563P.  
 PR 13-AUG-2002; 2002US-0406317P.  
 PR 15-AUG-2002; 2002US-0406182P.  
 PR 26-AUG-2002; 2002US-0406182P.  
 PR 26-AUG-2002; 2002US-0406355P.  
 PR 27-AUG-2002; 2002US-0406240P.  
 PR 12-SEP-2002; 2002US-0410084P.  
 PR 20-SEP-2002; 2002US-0412528P.  
 PR 23-SEP-2002; 2002US-0412731P.  
 PR 23-SEP-2002; 2002US-0414801P.  
 PR 30-SEP-2002; 2002US-0414839P.  
 PR 30-SEP-2002; 2002US-0414840P.  
 PR 30-SEP-2002; 2002US-0414954P.  
 PR 09-OCT-2002; 2002US-0417186P.  
 PR 09-OCT-2002; 2002US-0417406P.  
 PR 23-OCT-2002; 2002US-0420639P.  
 PR 28-OCT-2002; 2002US-0421156P.  
 PR 31-OCT-2002; 2002US-0422690P.  
 PR 01-NOV-2002; 2002US-0423130P.  
 PR 05-NOV-2002; 2002US-0423798P.  
 PR 05-NOV-2002; 2002US-0423798P.  
 PR 12-NOV-2002; 2002US-0425453P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Alsobrook JP, Alvarez E, Anderson DW, Boidog FL, Casman SJ;  
 PI Catterton E, Chapoval A, Crabtree-Boxer JR, Edinger SR, Elleman K;  
 PI Eitenberg S, Gangoli EA, Gerlach VP, Gorman L, Gunther E, Guo X;  
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;  
 PI Macschlian T, Malyanar UM, Mezick AJ, Mallet I, Mishra VS;  
 PI Padigara M, Patirajan M, Pena CE, Peyman JR, Raha D, Raselli L;  
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
 PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;  
 PI Zhong H;  
 XX  
 DR WPI: 2004-081935/08.  
 DR P-PSDB: ADH72216.  
 XX  
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
 XX  
 PS Example 54: SEQ ID NO 1111; 1880bp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide (NOVX). A  
 CC polypeptide of the invention has cytosolic, immunomodulator,  
 CC neuroprotective, anorectic, antidiabetic, antimicrobial, and  
 CC antilipemic activity, and may have a use in gene therapy, and as a  
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
 CC any of the 303 fully defined nucleotide sequences given in the  
 CC specification. The polypeptide is useful in the manufacture of a  
 CC medicament for treating a syndrome associated with a human disease. The  
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
 CC treating or preventing NOVX-associated disorder, e.g. cancer, cachexia,  
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
 CC diseases, metabolic syndrome X or dyslipidaemia. The nucleic acids are  
 CC further used as hybridisation probes, in chromosome mapping, tissue  
 CC typing, preventive medicine, and pharmacogenomics. The present sequence  
 CC encodes a NOVX polypeptide of the invention.  
 XX  
 SQ Sequence 10989 BP; 2700 A; 2872 C; 2781 G; 2636 T; 0 U; 0 Other;  
 XX  
 QY Query Match 41.2%; Score 4174.2; DB 12; Length 10989;  
 QY Best Local Similarity 64.8%; Pred. No. 0;  
 QY Matches 6407; Conservative 0; Mismatches 3358; Indels 118; Gaps 10;  
 Db 103 CTAGTCAAGAACCAATTGAGTGAAGTCTGAGGCTGAAGCTAGCCGCAAGAC 162  
 Db 1213 CAAGTGAAGAAAGCCGATTGAGTGAAGTCAAGAGGAGTCAAGATGCTCCAGCAAGAT 1272  
 QY 163 AACAGCCAGAAAGACGTGTGTAACTCAGGTGTGTGTCCCAAGACATAATATGTGT 222  
 Db 1273 GGAAGCCATAAAGAACTGTCTTGAGCCAGAGAGGTGTCATGTGTCTCATATGTGT 1332

QY 223 CCAAGCCTGGGATACCCGAAAGGGCAAAAGACTAGGCTCGATTTC---AGTTAGGA 279  
 DB 1333 CTAGATCCCTGGGATTCAGAAAATGTTGAAAGAGAGTTCCGACTTCAGTAAAGGTTGGT 1392  
 QY 280 TCCAGCGTCCAGTTCACTGCAACGAGGGCTATGACTCTGCAAGGGTCCAGCGGATCAAC 339  
 DB 1393 GCAAAATGTAACATTTTCAATGTAAGACAATTAACGTCTCCAGGGATCTAAAGATCAACC 1452  
 QY 340 TGTATGAAGTGAAGGACATGTTTCCGGCTCGGAGACGACCAAGGCGAGTCCGAGACC 399  
 DB 1453 TGTCAAGAGTTTACAGAGACGCTCGCTGTGGAGTGAACACAGGCCATCTGCGAGAG 1512  
 QY 400 CCGATGTGATGCCACCTTCGAGGCCCCCTCGGGCATATCACTCCCAATTTTCCC 459  
 DB 1513 AGAATCTGTGATCCAAATCTGGTGGGCCAGCGGCGTCACTTCCCTTAATATCCG 1572  
 QY 460 ATTCACTATGACAAATGCAATGCAACATCTGTGTGATCAATCAAGCACTCAACCCCTCCAG 519  
 DB 1573 GTTCACTATGAAGATATGCAACATCTGTGTGATCAATCAACCAAGCCGAGCAAG 1632  
 QY 520 GTGATCAAGCTCGCTTGAAGAGTTGATTTGAGAGGGGCTATGACACCTGACGGTC 579  
 DB 1633 GTCTATCAAGCTTGCCTTTTAAAGTTTGAAGCTGAGAGCGAGGCTATGACACCTGACGGTT 1692  
 QY 580 GGTGATGTGTCTCAGAGTGGGACCAAGAAAGATTCTCTACATGTTCTCAAAATGCTGAC 639  
 DB 1693 GGTGATGTGTGGAAAGGTGGGAGACCAAGATCGGTCTTGTACGTG----- 1737  
 QY 640 AGTGAACAGCCCTCAKACCCCAAGGCTCTCCATCCCAAGAGATGTCGGGACATCTGG 699  
 DB 1738 -----CTCAGGGATTCAGTTCTCAGCTCAT--TGTGACATGAGC 1779  
 QY 700 AGGCAAAATGACTGTACTTGAATCTGTCTGATGACATTAGCAATTCAGATSCAAAGTCA 759  
 DB 1780 AACCAATGTGGCTATCATCTGACAGTGAATGATGATGGCT----- 1822  
 QY 760 GGTTCAGTGAAGATCTCCAAAGACTTCTAATGCTGTGAACTTGTCTCTCGGAGACA 819  
 DB 1823 -----CACCTGGGTTTAAACCTGTTTACCA 1848  
 QY 820 GAGATCGAGAGGGGAGATTGCGGTGACCTTGACATCTGACATATGCGGAGGAAAGGC 879  
 DB 1849 GAATTTGAAAAGGAGGTGTGGGATCTTGGAATCCCGCTATGGAAGCGAGCGGC 1908  
 QY 880 TCCCGGTTTCAACCGGTGACACATCTCAAGTTGAGTGCAGCCCGCTTTGAGCTGTG 939  
 DB 1909 AGCAGTTTCTCCATGAGATACACTCACTTTGAAATGCCCGCGCTTTGAGCTGTG 1968  
 QY 940 GGAAGAAAGCAATCAATGCAAAAGATTAACCAATGTCGGCTAAGAAAGCAGGCTGC 999  
 DB 1969 GGGAGAGAGTTATCACTGTCAAGCAATCAATGATGATGCTGTGCAAAAGCCCACTGT 2028  
 QY 1000 GTGTTCTCTGCTCTTCACTTCACTTCAAGCAGCCGCTGTGGGTTGTCTGTCTCCCACTAC 1059  
 DB 2029 GTATTTTCAATTTCTTCACTTCAAGCAATCACTGTGGATTAATCTGTCAACCAATTAAT 2088  
 QY 1060 CCAAGAGACTATGCAACCACTCACTGTGTCTGTGCTCATCTGTGCGCAGGCGTGAAGC 1119  
 DB 2089 CCAAGAGAAATGGAACCAATGAACTGTGTGTGTTGATTAATCTGTGAGCAAGAAAT 2148  
 QY 1120 CGCATCCAGCTGGCTTCAAGCAATTTGAGAGCTCAAGTTGATTTCTGTGATTC 1179  
 DB 2149 CGAATTCACCTTAATCTTAAATTTGATTTGATTTGAGCTCAATTTGACTTTCTCGGGCTC 2208  
 QY 1180 AAGATGAGGCGACCGCGAGCGCGCTCTGTGGCACTTTCTAGAAACAGCTTCCC 1239  
 DB 2209 AAGATTAATGCAATTTTGAATTAATCTGTCTGTGGATCTTTTCTGTGCAATGAAGTCC 2268  
 QY 1240 TCTCTCAATCAAGAGATGCGCACTGTGCGCTCGAGTTCAGAGTGAACCACTCCACA 1299  
 DB 2269 TCCAGCTGGCCAGAGTGGGATTAATGTTGCTGTGAAATTCAGTCTGACATTTCCACT 2328

QY 1300 GGAAGAGGGGCTTGAATCACTTTTACCACTTCCAGACAAAGATGCCCCGATCT 1359  
 DB 2329 ACTGGACAGGGGTAAACATCACTTACACACATTTGGTCAAGATGATGCCATGATCT 2388  
 QY 1360 GGGCTTCAGTAAATGACAAACGTTTGGGAGACAGCTTCAGCTGGGAGCTCCATCTCC 1419  
 DB 2389 GGCATTTCTTAAGAGAGAGAGATTTGGTGAAGATTTCTTCTCTGGGAGCTCGGTTCT 2448  
 QY 1420 TTCTCTGTGATGAAGGCTTCTTGGAGTCAAGGCTCAAGAGACATCACTCGGCTGTG 1479  
 DB 2449 TTCTCACTGTGATGATGGCTTTGTCAAGACCCAGGATTCGATCTCAATTCCTGCACTG 2508  
 QY 1480 AAGAGAGGAGCGGTGTCTGAACAGCGGTGTCTGCGTGTGAAGTCCCTGTGTGT 1539  
 DB 2509 CAAAGAGGAGCTGTGTCTGAGAGCTCAACCGTGTGAGAGCTCACTGATGAGTGA 2568  
 QY 1540 CACCTGACTTCCGCGAGCGGACCATCTCTCTCCGGGCTGTGGCTGTCTTAAGAGAT 1599  
 DB 2569 CATCTGACAGCGTCCAGCGGAGTCAATTTGCTCTGTGATGAGCCAGGATTAATGAAGAT 2628  
 QY 1600 GCTTGAAGCTGTGCTGGGATGATGAGGCCAGCGGCTACCCCATCAAAATCACTTC 1659  
 DB 2629 TCTTTACATTTGAATGATTAATTTGAAGCAAAACAGGCACTTATCAAAATGACTTTT 2688  
 QY 1660 GACAGATTCAAAACGAGGTCAATATGACACCTGAAAGTACGCAATGGGCGGACTTAC 1719  
 DB 2689 GACAGATTCAGACAGAGGTCAATTAATGACACTTGAAGGTCAAGATGGGCGGAGT 2748  
 QY 1720 TCAAGCGCTTGAATCGGGGTTTACACAGGAGCCAGAGTTCCCAAGTTCCTCATCAGACC 1779  
 DB 2749 TCGTCCCACTGATCGGCGAGTACAGGACCCAGGACCCAGTTCTCATACAGACC 2808  
 QY 1780 AGCAATACCTTACCTCTCTCTTACCGACAGAGTCACTCGGACATCGGCTTCAG 1839  
 DB 2809 GGAATCTTCAATGATCTGCTGTTCACACATGACAAAGCGGCTTCAGATCGGCTTCTC 2868  
 QY 1840 CTCGGTATGAGACTATTAACATCTGACATGACACATCTGTGATCCAGAAATCCAGTA 1899  
 DB 2869 ATCCATATGAGATGAGCGTGTGATCGAATTCCTGTGTGAGCCGGGACATCCCTGTG 2928  
 QY 1900 AATGAGAGGCTCATGGAATTAATCTTAAGTGGGCGCGTGTGACTTCACTGTGAC 1959  
 DB 2929 AAGGCAATGCGCAGGTGAGACTTGTGATCAGATCCAGATGACATTTCACTGTGAC 2988  
 QY 1960 TCGGCTTACATTAATGAGCGGAGACTCTGAGATGTGAAGCCCACTTCCAGTGAAGC 2019  
 DB 2989 CCGGGGTACACATTAATGAGAGAGAGCCCTGTGTGTGAGAGGAAACACAGTGAAGC 3048  
 QY 2020 CGGCGCTGCGCAATTTGAGAGCTCTGTGTGTGAGCTTCAATTCAGGCTCCAGTGGAGC 2079  
 DB 3049 CAGCGCTTGCACACTGAGAGGCTGTATGTGAGGCTTACATCCAAAGGAAAGTGAACA 3108  
 QY 2080 ATCTGTGCGCAGGATTCCTGACTTACCCCACTTGAACCTGAACTGCACTGTGATTC 2139  
 DB 3109 GTCTTTTCTCTGGGTTTCAAGATTTTATCAAACTCTTAACCTGACAGTGAACAT 3168  
 QY 2140 GAATCATCTATGCAAGGATGTGTTCTTCACTTTCACACTTCCACCTGGAAGAGTGC 2199  
 DB 3169 GAAGTGTCTATGGAAGAGGATTCAAATGATCTTTCACACTTTCATCTTGAAGTTC 3228  
 QY 2200 CATGACTACCTCTCATCACTGAGAAAGGAGCTTCAACCCAGCCCTGAGGACATCACT 2259  
 DB 3229 CAGCACTATTTATCTGATCAAGAGATGGAAGTTTTCAGAGCCGTTGCAAGCTCAC 3288  
 QY 2260 GATCTCGGCTGCGACTCCATCAAGCGTGGGCTTAATGCAACTTCACTGCGCAGGTC 2319  
 DB 3289 GGGTGTGTGTGCTCATACATCAAGGAGGCTGTGTGAAACTTCACTGCGCAGCTT 3348  
 QY 2320 GCTTCAATTTCTGATTTTCTCATGCTCAATTAAGATTTCAACATCACTTCCAGAGTAC 2379  
 DB 3349 CGATTATATCAAGACTTCTCAATTTTGTAGAGAGGCTTCAATATCAATTTTCAGAAAT 3408  
 QY 2380 GACTTGAAGCCTGTGAGAGGCCAGAGTCCAGGCTCAAGACTCCGAGAGGCTTTCAG 2439

Db	3409	GACCTGGAGCCATGTGATGATCTTGGAGTCCCTGCTTCAGCCGGAAGATTGGTTTTCAC	3468
Oy	2440	TTTGGCGTGGGCGACACCTTGAACCTTCTCTGCTTCCCGGGATACCGTGTGAAGGCACC	2499
Db	3469	TTTGGTGTGGGAGACTCTCTGACGTTTTCTGTCTTCTGCGGATATCGTTTGAAGGTGCC	3528
Oy	2500	GCCCGCATCAGCTGCTCTGGGGGGGAGACGGGGCTGTGGAGTCCGCTCTGCCAGAGTGT	2559
Db	3529	ACCAAGCTTACCTGCTGGGTGGGGGGCGCGGTGTGTGAAGTGCACCTCTGCCAAGGTGT	3588
Oy	2560	GTTGCTGAGTGTGGGAATTCAAGTCAAGGCACTCAGGGGTACTTGGTCTGTCCCCAACTTT	2619
Db	3589	GTGCGCGAATGTGGAGCAAGTGTCAAGAGAAATGAAGAACATTACTGTCTCCAAATTTT	3648
Oy	2620	CCTGTGAACCTACAAATMACAATCATGATGATCTTACTCCATCCAGACCAGCCAGGAAAG	2679
Db	3649	CCATCCAAATTATGATATATACCATGATGATGTATCTATTAATATGAAGACGAAGCCGGCAG	3708
Oy	2680	GGAATTACAGCTGGAAGCCAGGGCATTTGGAATCTCCGAAGAGATGTCTCAAGTTTAT	2739
Db	3709	GGCATCCACCTTAGAACACGAAGCTTCCAGCTGTTTGAAGAGATACCTTAAGGATATAT	3768
Oy	2740	GATGGCAACAACTCCGGCCCGTTGTGGGAAGTTTTAGCAATTCGATATATGGGG	2799
Db	3769	GATGGAAAGACAGTTCTTCACTGCTCAGCTGAGGACGTTCACTAAATATGAATCTTGCGG	3828
Oy	2800	GTGACTTTGGAACAGACACATCCAGCAGCTGTGGCTTTGATTTTCAATCACTGATGTGAANA	2859
Db	3829	CTGATCCCTAAACAGACATCCATCACTATGCTATGAGTTTCAACCAATGATCTGAC	3888
Oy	2860	ACCAGCAAGGCTTTGAACTGCACTTTTCCAGCTTTGAATCAATCAATGTGAAGACCA	2919
Db	3889	ACCGACCAAGGTTTCAACTCACTCATACAGTTTGTGATCTGGTAAATGTGAAGATCCG	3948
Oy	2920	GGAACCCCAAGTTTGGCTACAGGTTTATATGAGGTCAATTTTGCAGGAGCTCCGTG	2979
Db	3949	GGCATCCCTTACTACGCTATATGATCCGTATGAAGGCCACTTTTCCGACACTGTACTT	4008
Oy	2980	TCCTTCACTGTGACCTTGATATACAGCTGCGGGGTATGAGAGACTCTGTCTGTAGT	3039
Db	4009	CTGTACATTTGCAACCCGGGGATGCCCATGATGACACACACCTTACTGTTTGAAT	4068
Oy	3040	GGAGAGCGCCGGAAGCTGGGACCGGCTCTGCCACCTGTGTGCCAGTGTGAAGGACA	3099
Db	4069	GGAGACAGAGAGTGTGGGACAAACCACTTCTGTGCATAGCGGAATGTGTGTGACG	4128
Oy	3100	GTGAGAGAGAGGTGTCCGGGCGAGGTGCTGTACCCGGGTATCCAGCTTCCCTTGAACAC	3159
Db	4129	ATCCATGAGCCACATCAAGGACGAATATGTTCCTCTGCTATCCAGCTCCGTAATGACAAAC	4188
Oy	3160	AATCCAACTGCATGTGACCATGGAACAGAGGCGGCTGACCATTTGGGCTACACTTC	3219
Db	4189	AACTTCCACTGCACCTGGAATTTATAGGCGAGCCAGAAAGAACATTATAGCTTCAATTTCC	4248
Oy	3220	CTGTGTATTGACACAGAGAGGTTTCACGACGTGTCCCATCTGGGATGGGCTGTGGAG	3279
Db	4249	ATTGTTTTGACACGGAGATGGCTCAGACATCTCAAGGTCTGGGACGGGCCGGTGGAC	4308
Oy	3280	AGCGGGGTTTCTGTGAAGAGCTGATGTGGCCCGGCTCTGGCCAMAGACTGTGATAGCAC	3339
Db	4309	AGTGACATCTCTGCTGMAAGAGGTGAGTGGCTCCGCTTCCGAGAGCATCACAGCACCC	4368
Oy	3340	TTCAACTGGGTGCTGTGCACTGTCAGCATCTTCAACAGACAAAGGCGTTTGGC	3399
Db	4369	TTCAACTACTACCTCTGAGTTTGCACACGCACTTCTTCAATGCAATCTGTGGCTTCTCC	4428
Oy	3400	ATTCAATTTTCAAGTGTCCACAGCAACGTCTGCATGACCTGTGGATCCCGCAGATATGG	3459
Db	4429	ATCCAGTTCTCCACTCAATTGAGACCACTGTAAACGATTCACAGATATCCCCAAATATGC	4488
Oy	3460	AGTCCGAGTGTGACAGTTGGGAGCCGGCGAATTCACAGTGTTCAGTGTGACCTTGGC	3519

Db	4489	ACC	GCTATGGAGACAGACGAGAGGCTGGAGAACACCGTCACTTCAGTGTGACCCCTGGC	45458
OY	3520	TAC	CGCTGCAAGGAAAGTCAGAGATGACTGTGTGAAGATCGAAGACAGTTCTTCTGG	357979
Db	4549	TAT	CAGCTCCAAAGGACAAAGCCAAATATCACTGTGTGACGTGAATTAACCGGTTCTTTTGG	46080
OY	3580	CAG	CCCAAGCCCGCCAAACATGATGCTCCCTCGGGGGGAGACCTGACAGGACCAATCTGG	36399
Db	4609	CAAC	CAGACCTCTTACATGATATGCTGTGTGTGAGAGGAATTCGACGGGCCACAGGT	46686
OY	3640	GTC	ATCCCTCACCAAAATTACCCAGAAACCTTACCCCGCAGGACAGAGTGTGACTGAAA	36899
Db	4669	GTT	ATTTTGTGATACCAACTACCCACAGCCGATCTCTCTGGGAAGGAATGTGACTGGAGA	47280
OY	3700	GTC	ACCGTCTCACCAGACTACGTATGCGCTGTGATTTAAACATCTTAACTTGAAGCT	37599
Db	4729	GTA	AAAGTGAACCCGGACTTTGTGTATGCTCGCTTGTATTTCAAAATTTCATATGAGACCC	47880
OY	3760	GGC	ATATGATCTTCTTCCATATCTTAAGACGGACGGGACCTCTCAGCCCTCTCATAGAAAC	38199
Db	4789	AGC	ATATGCTTCCATCACTATTAAGAGGGGAAATTTCCAAACGCCCCCTATTGGAGGT	48480
OY	3820	TTT	CTATGGCTCCCAAGCTCCCAAGGCCGCAATTGAAAGACAGACAGACTTTCCTGACC	387979
Db	4849	TAC	CAGGCTCTCAGGCCCCCAAGAAATAGAGTACGGAAACAGCCTGTCTTGGA	49080
OY	3880	TTT	CGCAGCAGTGCATCTGTGAGCAATGCTGGCTTGTGATTCATGCTATACGAAACCCG	39399
Db	4909	TTT	CGAGATGATGCTCGTGCGCTTCAAGGGTTTGGCATTGAATTTAAAGAAACCA	49680
OY	3940	CGG	AGTCAATGTTTGGATCTGTTCATCAAGAACGGCACAGGGTGGGCTCCGACTGT	39999
Db	4969	CGG	AAGCTGTTTGGACCCAGGAAATATATGATGGGACAAAGTTGGAACAGACTTC	50280
OY	4000	AAG	CTGGCTCTCCGCTACCTTACTACGCGACGGGGCTTACGAAATTTGAGGGACCTCG	40599
Db	5029	AAG	CTTGCATCACTGATGATTTGGGGCTGATGAGGAAACCTCTCTGGGACCAAGTCTGCCCTC	51480
OY	4060	ACC	CTGACTGCTGAGGCTGATGAGAACGCCGTGTGGAACAATCCCGGCGACATC	41199
Db	5089	TTC	ATCACTGTGTGATTTGGGGCTGATGAGGAAACCTCTCTGGGACCAAGTCTGCCCTC	51480
OY	4120	TGC	CAGCCCCCTGTGGGGGACAGTATGTGGGTTCCGACGGAGTGTCTTCTCCCAAC	41799
Db	5149	TGC	ATGTCTCTCTGTGGAGGCGACATTAACGGGATCAGAAAGGGGTATGTTTATCAACAAAC	52080
OY	4180	TAC	CCCCAGACTACACCAAGTGAACAGATCTGCTGATTTTGTATCTGTGCCCAAGAC	42399
Db	5209	TAC	CCCCATAATTAACACAGCTGTGCAAAATATGCTCTATTCATCAACGGTACCAAGGAA	52680
OY	4240	TAT	GTGTGTTTGGACAGTTGCTGCTTTTCAACAGGCCCTCAACGAGCTGTGGAGGTT	42999
Db	5269	TTG	GTGTGCTTTGGACAGTTTGGCTATTTTCCAGACAGCCCTGAATGATTTGGCAAAATTA	53280
OY	4300	CAG	CAGCAGCAGACACGACTGCGGGCTCTCACTGCTCTGGGCTCCCATACAGA	43599
Db	5329	TTT	ATGATGAACCCATGACAGGCGACAGACTTCTCAGCTCACTCGGGGTCTCACTCAAGG	53880
OY	4360	GAA	TATCATCTGCCCCCTTGGCCACTCCAAATCAAAATTTGTGCTCGATTCAGTGCMAAGCGGT	54480
Db	5389	GAA	CATTGCTTGGCTTGGCTACGTCAAAATCAAAATTTGTGCTCGATTCAGTGCMAAGCGGT	54480
OY	4420	GCA	CCAGCAGAGGCTTCACTTTGTCTTACCAACGGGTTCTCTGAACAGGCGCACAG	44799
Db	5449	GCT	CTTGGCGGGCTTCACTTGTGTGTATGACGTGTCTCTGTACCAAGTGAACCCAA	55080
OY	4480	TGC	AGCTTGTGCGGAAACCCCGCTATGGAAGAGGCTGGCAGTGAATTTCTCGTGGGG	45399
Db	5509	TGC	AGCTTGTGCGGAAACCCCGCTATGGAAGAGGATTTGGTCTGAGTTTCTGCGGGC	55680
OY	4540	GCA	TCTGCTCGCTTCTGAATGCAATCTCCGGCTATGACCTCTGACAGGGGTGCGCAGATGAG	45999
Db	5569	TGC	ATGTCTCGCTTCTGAATGCAATCTCCGGGATCACTGTCTTCAAGGGTTTCAACGGCGCTCAC	56280

QY 4600 TGCCTCCCTGTGCTGGGGCTTTGGCCCAATGGAATGTCAGCGGCCCAAGTGTGGTG 4659  
DB 5629 TGCAGATCCGTGCCCCAAGCCTTGGCAAGTGAACAAGATCCCAAGCTGTGTGTA 5688  
QY 4660 CCGTGTGAGGCAACCTCCAGAGCGGAGCCATCTGTCCCTGCTTCCCAAG 4719  
DB 5689 CCTTCAGTGGCAATTTCACTCAAGMAGGTACATCTGTCCCGGGCTACCTGAG 5748  
QY 4720 CCGTACCTACAGCCTCAACTGTGTGTGAAGATGTGTGTCCCGAAGGGCTGGCA-T 4778  
DB 5749 CCATACGGAACAACCTTGAATGTATAGGAATCATATGTTACGAGGGCTCGGGAAT 5808  
QY 4779 CCAAGTCCAGTTTTCAGTTTGTGACAGAGCAAGCTGGGACT--CGTGGAGATATTT 4836  
DB 5809 CAAGATCCAGTGTATGATGTTGGCCAGAGCAAGCTGGAGCTTCCCTTGAATCCAC 5868  
QY 4837 GATGTGACATTAACCTGTAACTGTAGCTGGGAGTTTCTCAGAAACAACGCTGCTGCC 4896  
DB 5869 GATGTGGGGATGTAGCCGCAACCGACCTGGAGAGTTTCTCAGGCAACAGTACCGCA 5928  
QY 4897 GTTCTGAACAGCACTCCACCAAGCTTACCTTCACTTCTACTCAGATATCAGCTATCT 4956  
DB 5929 CTGCTGAACAGTACTTCCAACTCACTCACTTCCAGTGTGACATTAAGTGGCA 5988  
QY 4957 GGAGCTGGCTTCACTTGGAGTACAAAACGTTGGGCTGAGCAGTTGTCCGGAACCTGCT 5016  
DB 5989 GCTGCTGTTTTCACCTGGAAATACAAACTGTAGGTCTGTGCAATGCCAAGAACAGCC 6048  
QY 5017 GTGCCAGTAAACGGGTGAAGACTGGCGAGCGCTACTTGTGATGATGTGTCTTTC 5076  
DB 6049 CTCGCCAGAACAGCATCAAAATCGGAGATCGGTACATGTGTAAACGAGTGTCTCTTC 6108  
QY 5077 CAGTGTGACCCGGGATATGCTCTCCAGGGCCAGCCCAATCTCTCTGATATGCCCGGAACA 5136  
DB 6109 CAGTGTGACCCGGGATACACCTCGAGGGCGCTTCCCACTTCTGTATGTCAGAGGACC 6168  
QY 5137 GTGGCGGAGTGAAGTAACTACCTCTCTCACTGTATATGACAGTGTGGGGGAACAGTGGAG 5196  
DB 6169 GTTCCGCTTGAACATATCT 6228  
QY 5197 GAGATGAGGGGTGATCTGTAGACCCCGGCTTCCAGGCACTACCCCAAGTAACTGAC 5256  
DB 6229 ACCTTGGGTGTGTGATCTGTAGACCCCGGCTTCCAGGCTTCTTAACTTCACTTAC 6288  
QY 5257 TGTCTCTGAAAAATPACACTGCCCCGGGCTTGGAGCTCACAATCCAGTCTCTGAACTTC 5316  
DB 6289 TGCACCTGAGAGTCTCATTTAACCATCGGCTATGTGCAATATTCAGTTCTGAAATTT 6348  
QY 5317 TCCACGAGCCCAACACGACTACATAGAAATCCGGAATGGCCCTATGAGACAGCCGC 5376  
DB 6349 TCTACGGAAGTATATGATCTTCTTGAATTCABAATGGAATCTTACACACAGCCCC 6408  
QY 5377 ATGATGGGAATTCAGTGAAGCGAGCTTCCAGCTCCCTCTCTCTCTCTCTCTCTCTCT 5436  
DB 6409 ATGATGGCAATTTAGCGGCAAGATCTCCCGCGCCCTGTGTAGCAACAAGCATGAA 6468  
QY 5437 ACCACGCTGATTTCCACAGCGCACTCCCAAGATCGGCAAGGATTCAGCTGAGTAT 5496  
DB 6469 ACCCTATCCACTTTATATGTGACATTTGCAAAAACCGGCAAGGATTTAACTTGTATTC 6528  
QY 5497 CAGGCTATGAACCTTGAAGAGTCCAGAACCCAGAGCCCTTGGCAATGGCATTTGTAG 5556  
DB 6529 CAGGCTATGAATTTACAGAACTGTCCAGATTCACCCCAATTCAGAAATGGGTACATGATC 6588  
QY 5557 GAGAGCTGACTAACAGTGGGACATCATGATCCTTGAAGTGTCTCCCGGGATATCAATTG 5616  
DB 6589 AACTCGGATTAACAGCGTGGGCAATCATGATCTTTGAGGTATCTCTGGGTACATTTCA 6648  
QY 5617 ACTGGCAACCTGTCTCTCAAGTGAACATGAGCAACACGGAACCTGGGACCAACCCCTG 5676  
DB 6649 ATAGGCCATCTCTCTCACTTGTGAGATGGAATCAACAAAACCTGGAATCACTCTTTT 6708

QY 5677 CCAAGTGTAGATCCCTTGTGGCGGGAACATCACTCTTCTCAACGGCACTGTGTACTCC 5736  
DB 6709 CCAAGATGTATGCCCTTGTGGGTACAAAGTAACTTCTCAGAAAGGCAACCATCTACTCC 6768  
QY 5737 CCGGGGTTCCCTTACCCCTGATCTCAGCTCCAGAGATGTGTCTGTGTGATCACCCTGCC 5796  
DB 6769 CTTGGCTTCTTATGATGATTCGATCTCGAAGAGATGCAATTTGGCTCATACGGTCTCT 6828  
QY 5797 ATTGGCATGGCGCTCGCTCAACCTCAGCTCTGTGACAGAGCCCTCTGAGATTTTC 5856  
DB 6829 CCAAGGCAAGGATTTATCATCACTTCACTCTGTACAGAGGAGCTGTCAAGATTTAC 6888  
QY 5857 ATCAACATCTGGAGTGGGCCACAGCAACCAAGCTCGGCTTTCACCCGAGC 5916  
DB 6889 ATTGCTTTTGGAGCGGTCCGATTCAGAACTCACCCCAAGCTGGAGATTTTCAGTGGCAAC 6948  
QY 5917 ATGGCCAAAGAAACATGTGAGAGTTCATCCAAACAGGTCTGTCTCAAGTTCCACCGGAT 5976  
DB 6949 ACAGCCTCGAAACGGGGTATAGTCCACCAACCAAGTCTGTCAAGTTCCACAGGAC 7008  
QY 5977 GCAAGCAGAGGGGATCTTCCCAATAGCTTCTCCGCTTATCCACTCACCAATGCTCT 6036  
DB 7009 TTTTCAATGAGAGCTTCTTGTCTCAATTTCCAGCATTTCAGCTCAAGAAATGTCAA 7068  
QY 6037 CTTCCCAACATCTCTCCCAACGCGGAAGTGTCAAGAGATGAAGATTCATATAGT 6096  
DB 7069 CCTCCCAAGGGTTTCCACAGGCAAGAAATGCTTACTGAGATGATGTATTCGAATAGGA 7128  
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QY 6157 TGCAAACTTGGAACTTACCTGAGTTTGAAGAACCAACCCCGATATGTGAATGCTACTGT 6216  
DB 7189 TGCAGCTCACTTCCAGTGTGAGTTGAGGGTTCTCTCCCAATGTGAAGCAATATGC 7248  
QY 6217 CCAACAAATGAGCTTCTGACAGACTCCACAGGCTGTATCTGAGCCAGAGTACCTTGA 6276  
DB 7249 CCAGCAATGAAAGTCCGAGCTGTATCATCGGAGTCACTTCACTCAGGGTATTCGGGT 7308  
QY 6277 AGCTATCCCGCTTCCAGACCTGTCTGTGGTGTGAGTGGAGCCGACTATATATC 6336  
DB 7309 AATTTATTTTAACTCCAGACTGTCTTGTGATTTAAATGGAACCAACTACATTA 7368  
QY 6337 TCCCTCAGTGTGATCTTCTCAGAGAGAAAGCAATATGATGATTTTGTAT 6396  
DB 7369 ACATCTTTGTGACACATTTCAAAAGTGAAGAAAGCATTTGATGACGTGAAGTGTGAT 7428  
QY 6397 GGTCAATGAGACAGAGTCTCTGTGAAGCCCTCAGTGGGAATTTACTAGCTCCCTG 6456  
DB 7429 GGTCTTCTGGCAAGTCTCTGTGTGTGTATTTAGTGGGAATCATCTGAACATCA 7488  
QY 6457 ATTGTACAGCTCAAGCACTGTGTATCTGTGATCTGTGTGTATCTGTATCAAGCTTACAT 6516  
DB 7489 AATTTTACAGAGAGATATCAATATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7548  
QY 6517 CGAAAGGCTTCAAGATCCGCTATTCAGCCCTTATCTGACAGCTTGCAGGGCTTCACTC 6576  
DB 7549 AAGAAAGATTCAGATTCGCTATGACAGCACTTACAGTGTGACCAACCCCTGAG 7608  
QY 6577 CATGCTTATCTTATGAGCAACAGACCAAGCCCGGGGCTCATCTTTGGCTGC 6636  
DB 7609 AATGGGGTATTTTAAACAGAGCTGACAGAGCGGTGGAACAAAGTCAATATTTTGTG 7668  
QY 6637 AACGGGCTACCGCTGTGGGACACAGATGAGCAATCTGTACCCGGCAACCCCAAGGC 6696  
DB 7669 AAGCTGTATACAGATGTGTGGCCACAGCAATGCAACTGTATACAGAAACCACTTGGC 7728  
QY 6697 TACCACTGTGAGGAAGCAATCTCTGTGTGAAGCTCTTCTGTGTGTGTGTGTGTGT 6756  
DB 7729 ATGTACAGTGGAGTCCCTCAGCCCACTGTGCAAGGCTGTGTGTGTGTGTGTGTGTGT 7788  
QY 6757 GCCCCCAAGAAATGGAATGTGTGTGTGGCAAGAGTACACAGTGGGAACCAAGCGGTGTAC 6816

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Db      7789  TCCCCGAGAAACGGTTCATTACCGGGAGAGAGTTCACTTGGACAGTAAGGTCCTAT 7848
Qy      6817  AGCTGAGTGAAGGCTTACCACTCCAGGAGGGGCTGAGGCCACTGACAGTGTCTGAC 6876
Db      7849  GAATGTCATGAAAGGCTTCAAGCTTGAATCCAGCCAGACAGACAGCCGTTCTCAAGAA 7908
Qy      6877  ACAGGCTTATGAGCAACCGCAATGTCACACAGTGTGCTGCTGACTTGTCTGAT 6936
Db      7909  GATGGCTGTGAGTAACAAGGGGAAGCCGCCATGTGTAGCCGGTTCCTCCAGC 7968
Qy      6937  GTCAATGATCAACCGTGAAGATGGCCGATGAGGCTTATCTTTGACACAGTATCAG 6996
Db      7969  ATTGAAGCTCAGCTTCAGAACATGTATCTGAGAGCTGGTTCAAGATCTTGAATGAG 8028
Qy      6997  TTCAGAGCCGAGTATGCTCATCTGTGACCCCTGGCTACTACTATCTAGCCAAAGGTC 7056
Db      8029  TACGGTCTCAAGTATTTGAGCTGACGTGCTGTTACTTAAAGAGGCTGGAGGCTC 8088
Qy      7057  ATCCGCTGTCAAGGCAATGAGCAATGAGGCTGGGGGACTCTAGCCCACTGCGAATC 7116
Db      8089  CTGCGGTCCAGGCCCAATGGGACGTGGACATAGAGATGAGAGGCCAAGCTTCCAGTT 8148
Qy      7117  ATCTCGTGTGAGAGCTCCCGATTCGCCCAATGGCCACCGCATCGGAACACTGTCTGC 7176
Db      8149  ATCTCGTGTGAGAGCTTTCCTTCCCGCAATGGCAACAAATGGAAAGCTTGACAGTT 8208
Qy      7177  TACGGGGCAACAGCCACTTCTCTCTGCAATCCGGATATCACACTGTGGGCTCAAGGTG 7236
Db      8209  TATGGGGCCACACACTATATTATAGTGTCAACACGGGCTACACGCTTGTGGGCTCATGTC 8268
Qy      7237  CGTAGTGCATGAGCAATGGGCTCTGGAAGTGGCTGAGTCCGCTGTGCTGAGCAC 7296
Db      8269  AAGAGATGCTTGGCAATGGGCTCTGGAAGGCGAGGAACTGATGTTTAGCTGGCCAC 8328
Qy      7297  TGTGGACTCTCGAGCCCATTTGTCAACGGAACATCATCATGAGGAGAACTACAGCTAC 7356
Db      8329  TGGGGTTCGCCAGACCCGATGTGAAACGGTCATTAATGAGATGGCTTCACTTACAG 8388
Qy      7357  GGGAGTGTGTATCCAAATGCAATGCTGCTTCCGCTGATCGGCATGTCTGTGCGCATC 7416
Db      8389  GATACGTGTGTATCCAAATGCAATGCTGCTTCCGCTGTGTGGAACTTCCGTGAGAGAA 8448
Qy      7417  TGGCAGCAGGATCATCATGCTGTGGGCAAGACCCCTTCTGTGTCGAATTAACCTGAG 7476
Db      8449  TGGCTTCAGAACCAAGTGTGTGACAAACGCTGTGTGTCCGTATCAATGTGTGT 8508
Qy      7477  CACCCAGGCAACCTGTCTCAACGCGCTCACTCAGGGTAAACAGTTTAACTCAACGATGTG 7536
Db      8509  CACCCAGGAAACCTGTCCACGGAATTCATTAATGAGCAGTGAATTTCAACTGATGATGC 8568
Qy      7537  GTCAAGTTTGTGTCACACCTGGGTATATGCTGAGGGGGCTGTAGTCCCAATGCTG 7596
Db      8569  GTGAATTTTCACTGTCAACAGGGGCTATTGCTGCAAGGGCGTGTCTGAGGCCAGTGTG 8628
Qy      7597  GCCAGGGGGAATGAGTGAATGCTGCCCACTTGCAAGATCATCAATCTTAAAGATTCCT 7656
Db      8629  AGCAAGGGCCAGTGAAGTACCTTGTGCCACGATGTGAGTGAACGTGTCTGTATCCA 8688
Qy      7657  GGAACAAGAAATAGTGTCTGTCAAGTTCACGCGAGCGGCGGACAGAGTTCACTTC 7716
Db      8689  GGGCTTTGTGGAATAATGCAATTCCTCAAGGCAACAAATCTTCCCTAGAGTTTGTGATAT 8748
Qy      7717  GGCACACTGTGTCTTACCGGTGCAACACGAGCTTCTACTCTGTGGGCAACCCAGTGTCT 7776
Db      8749  GGAATAGTATCTGTACCATTTGCAAGAAAGGATTTTACTGTGCGGATCTTCAAGCTTG 8808
Qy      7777  AGCTGACAGGAGATGAGCAATGGGACCGTCCCGGCGGCGGAGTGTCTTGTGTGTCTGT 7836
Db      8809  ACTGTATGCAATATGCTTATGGAGCCATCTTCCCAAGTGTGTGCTATATGTGTGT 8868
Qy      7837  GGCATTCGGGCTCCCCGCTCACTCCAGATGTCTGAGACAGTTATACTGTGGAGGAC 7896

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Db      8869  GGAACACCAAGGGTCCCTGCAACGCCGCTCTCATCTGAGAGCTGTTTACTATAGCGCC 8928
Qy      7897  GTGTGCGGATCAGAGTGCATTCGAGCAAGCGTACTGTGTGGGAAACAGACCCGATGTGT 7956
Db      8929  GTGTGTACTTACTCTGTGAGAGGAGCGAGAGCTTATATGGAACCAACAGAGTGTGTC 8988
Qy      7957  GGGCTGATATGACACTGAGACTGAGCTCCCTCCCTCACTGCTCAGGAACAGCGTGGAGTT 8016
Db      8989  CAGGAAGACAGTCACTGAGAGCGGGGCACTGCCCACTGCAAGAAATAATCTGTGATTC 9048
Qy      8017  TGGGTGACCTCTGGGATCCCGCTCATGAGCAATCCGTTGGGGGACAGCTTTGATCCAGC 8076
Db      9049  TGTGTGATCCGGGGGACCCAGACATGAGTGTCTGGCTGTGTGATCACTTTAAGACMAAG 9108
Qy      8077  ACTGTATGCGGCTTCACTGTGAAGCTGGGCAAGTGTCCGGGGATCGTCAAGCGGACAC 8136
Db      9109  AGCTTCTCCGCTTCTCTGTGAATGGGGCACAGCTGAGGGGCTCCCTGAACGACAG 9168
Qy      8137  TGTCAAGCCAAATGAGCTCGTGAAGCGGCTGCAAGCTGATGTGAGTATCTTGTGGG 8196
Db      9169  TGTGTGTCAATGGGTCATGTGTGAGGATCTGACGCGGTGTGTGAGCGCGTCTGTGGC 9228
Qy      8197  AACCTGGGACTTCCAAATATGCGCGAGTGTGTGTCAATGATGTGCTGATTTCTCCAGC 8256
Db      9229  AACCTGGGACACCCCAACGAAATGATTTGATGATGATGAGATGGCATTTCTGTCTCCAGC 9288
Qy      8257  TCTATGCTATATGAGTCCGGGGAAGATATCTAAGCCACAGGCTGTCTACCGCTCATC 8316
Db      9289  TGGGTATATATGCTGTGGGAAGGCTAACAGACTCAGGGCTCATGACAGGCAATTC 9348
Qy      8317  TCGGTCAATGTATACCTGACAGGAGTACCTGAGTGCCTGCTCAATACTGTGGTAC 8376
Db      9349  ACAGCCAAATGGGACCTGAGACAGGCACTGCTCCGACTGACAGATTAATGTTGTGGGAT 9408
Qy      8377  CCGGATTCACCAATGAGGCTTCGGCTGGGCAATGACTTCAAGGTAACAAACAACTGTG 8436
Db      9409  CCAGGCACTATGACAAATGGCATTCAGTTTGGGACCGAATTCACCTTCAACAAAGCTGTG 9468
Qy      8437  ACATATCAATGTGTCCCTGCGCTATATGATGAGTCAATAGATATCTGTGCTGAGCTGC 8496
Db      9469  AGCTATCAATGTATCCCAAGGCTATGTCAATGAGAGTCAATCCGCACTATTCGCTGT 9528
Qy      8497  ACCAAGGACCGGACATGGAATGAAACCAAGCCGCTGTGCAAGACTCTCATGCAAGCA 8556
Db      9529  ACCAAGAGCGGAGTGAATCCGAGCAACCTGTCTGAAAGCCGTGTGTCTCTCAG 9588
Qy      9589  CCGCGCGGCTGCAAGATGGAACATGTGAGGGAATTTCCGCTGGGGCTCCAGCATAT 9648
Db      8617  ACTTATGCTGCTGTGAGGGGTAACAGCTTCTCCCTGCGCGGTGTTCACTGTGAGGA 8676
Qy      9649  AGTTACAGCTGATGAGACGTTACCAAGCTTCTCACTCCGCACTCTCTCTGTGAAAGT 9708
Db      8677  AATGGTCTGTGACCGGAGAGTGCCTGATGTTTCCGTGTTCGCGGGATTCCTGTGT 8736
Qy      9709  CCGGGGTGTGAAGAGAGATCCCAAGTGTCTGCTGTGTCTGCGGAGACCTGTGC 9768
Db      8737  GTCCGCTCCGTTGGAGAGAGAGACCGAGGCTTCTCTTACAGGTCATCTGTCTCTTC 8796
Qy      8797  TCTGTGCATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8856
Db      9829  CAGTGAATCTTCCATTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9888
Qy      8857  ACATGAGTGGACCAAGCCAGCTGCAAT---AGATCCGACCTGACCAAGTGTGAGC 8913
Db      9889  AGTGAAGGGCAATACACACCTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9948
Qy      8914  CCTGTGTGCCACAGTTTGGGATTAAGAAATTTCTCAGGGGCTTACAGGTTGGAAGCACA 8973
Db      9949  CCGGTAGCCACACTTTGGAATTAAGAAATTAAGTCAAGAGGCTTATGAGGTTGGAAGCAG 10008

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OY	8974	GTCCCTTCGCGTGTCAAAAAGGGCTACTCGTTACAGGGCTCAACACAGACCTGCTC	9033
Db	10009	GTTTTTTTCAGGTGACGAAAAGGCTCACATATTCAGAGTTCCAGACTGCGACTGTGCTTT	10066
OY	9034	CCAAACCTGACCTGAGTGAACCCCACTGACTGTGTCCCAACCACTGACGAGCGCA	9093
Db	10069	GCCAAATTAAATCATGAGAGTGGGATATACAGACGAAATGTATATGTCATGCTCTCAGACGCA	10128
OY	9094	GAGAGCGCAACGCATGCCAAGTGGGGGCCCTGGATTTGGCCCTCATAGGGCTACAGCTC	9153
Db	10129	GAAACCCCGGACACGGGAGTGTAGAGCCATGATCTTCTTCTTTCGGCTACACTTA	10188
OY	9154	AT-TACTCTCTCCAGAGAGGCTTCTCCTCAAGGGTGGCTCCAGCACCCGACCTGCAAG	9212
Db	10189	GTTGATCACCTGCCATCCAGGCTTTTCTCGCAGGGGGATCTGAGCACAAATGTAAA	10244
OY	9213	GCGGATGGCAGCTGACAGCGAAGCCGCCCATCTGCTGAGGTCGGGCCAGTGGAGA	9272
Db	10249	GCAACATGAAATGAGACAGAAATGCCCTGTGT-----GTAAAGT	10299
OY	9273	CCCATCAACACTGCCCGGAGCCACCGCTACCCCAACCTGATTCCTGGGGATGTTTTT	9332
Db	10291	AAAGAGTGAAGAAAGTTAAAGAAACGTATCAAACTCCAGTCTCTCAGATGCTTT	10355
OY	9333	GCCAAAGATTCCTCTGTGGAAAGGGGCTATGAATACAGGGGAGAAAGCAGCAGCATG	9392
Db	10351	TTTCGTCAATTACGTGTGGAGGGGTATATTAATATTTAGGAAAAGACACCGGCACT	10410
OY	9393	CTCAGAGTGACTGCTTCCAAATTGCCAAGCAGCAGGTCAATGCCACATGATGCACAC	9452
Db	10411	CTAATCTGTGACTGTGTTCAATGCAACAGCAGTAAAGGTGAATGCCACTTCAACGAAAGCC	10470
OY	9453	AGTGGCGGTGAGCTGCACCTGGGCTGGAACCTTACAAGAAAGATTTTCACTCCACTC	9512
Db	10471	TCCGCAGTGGAGCTGAAGTTGACAGGCATTTACAAGAAAGAGAGGCCCACTTACTCTG	10533
OY	9513	CAGGTGTAACCAATTAACAGGGCTGTGAGATCTTTATGATTAAGTTCAAAAGATGATCA	9572
Db	10531	AAAGCTTTCAAAATTAAGGCAAGGACAGATATTTTTGTAGCAAGTTCGAAATGACAC	10599
OY	9573	TGGGCTTTAATATGGCATATCTCGTCAGAGTCTCCGAGCACCTTCAATCTACAAAGC	9632
Db	10591	TGGGAGACTAGATGTATATGTCTACTCTGGACTTGAAAGAGAGATTTACTTTTCAAGGT	10650
OY	9633	TCTGTCAAAGGACCAAGGCTTTGGGACAGTGGGCTTTCAAGAAGCTGAGGCTGAGGCTG	9692
Db	10651	GACATCTATGSAAGACTTTGGAAAAATTTAAGTTAAGTAAAGGCAAG-----TCTTTA	10704
OY	9693	GAGTCAAGCCCGAGTCAATTGGCCGCACTTGGCTTCCAACAGCAGCTCAGTGGGAGCC	9752
Db	10705	AAACCAGATCAAGACTCTTCCAGTCATTAACAAGGACACAGCAGTGGCTGTGGGGGCT	10766
OY	9753	GCGATCTCTGTGCTTTTCATGCGCCCTCATTTATGGGGCTTGTGCTATCTCTACAG	9812
Db	10765	GCCATTTCTGTCTCTTTCTTGTCTCTAATTTTACAGGGTTTCATTTTACCTCTCAAA	10824
OY	9813	CACAGAGAAACCCAAAGTCTTTCAATGGCTATCTGGCCAGCAAGAACCAATGTT	9872
Db	10825	CACAGAACGAAACCAAAAGTTCAATACATGGCTATGCTGGCATGAAAACAGCAATGGA	10888
OY	9873	GGGGCAATTTTGAAGCCCAATGACGACCGCAATCCAGCCCAAGACATCATGGCC	9932
Db	10885	CAAGCATGTTGAAAAACCCCATGTATGATCAAACTTAAACCCACAGAAAGCAAGGCT	10944
OY	9933	AGCGAGGGGAGTTCAAGTCAGACAGTGTGCAACAGCAATAT	9975
Db	10945	GTCAGGTTTGCACAACTCTGAACAGCTGTGACATGTGAT	10987

RESULT 14  
AAD33320  
ID AAD33320 standard; cDNA; 10433 BP.

Accession	Gene	Location/Qualifiers
AA033320;		
01-JUL-2002	(first entry)	
Human C3b/C4b complement receptor like cDNA #2.		
Human; C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; multiple sclerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischemic condition; noctropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiac; gene; ss.		
Homo sapiens.		
Key	Location/Qualifiers	
CDS	1..9303	
FT	/*tag= a	
FT	/product= "Human C3b/C4b complement receptor like protein	
FT	#2"	
FT	/note= "CDS does not include start codon"	
FT	/transl_except= (pos:2176..2178, aa:Xaa)	
FT	/note= "This translational exception occurs while	
FT	decoding the alternative version of human C3b/C4b	
FT	complement receptor like protein #2 (AAE20901)"	
FT	/partial	
MO200210199-A2.		
07-FEB-2002.		
24-JUL-2001; 2001WO-US023232.		
02-AUG-2000; 2000US-0222504P.		
28-NOV-2000; 2000US-00728787.		
(AMGE-) AMGEN INC.		
Welcher AA, Elliott GS;		
WPI; 2002-303934/34.		
P-PSDB; AAE20789; AAE20901.		
Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, and multiple sclerosis.		
Claim 1; Fig 2; 251pp; English.		
The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischemic conditions, metabolic disorders (e.g. obesity and diabetes) and infertility. The invention is useful in gene therapy. The present sequence is human C3b/C4b complement receptor like cDNA		
Sequence 10433 BP; 2618 A; 2671 C; 2527 G; 2610 T; 0 U; 7 Other;		
Query Match	40.1%; Score 4067.4; DB 6; Length 10433;	
Best Local Similarity	65.5%; Pred. No. 0;	
Matches 6001; Conservative 5; Mismatches 3136; Indels 25; Gaps 3		
819 AGAATGACAGAGGAGGAGTTCGGTGAACCCGATACCTGATATGCGCGAGGAGG 878		
168 AGAAATGAAAGGAGGAGTGTGGGAGATCCCGATCCCGCTATGCGAAGCGGACGG 227		



QY	879	CTCCCGGTTTCAACAAGGAGACACTAAAGTTTAAAGTCCAGCCCGCTTTAGAGTGT	938
Db	228	CAGCAGTTTCTCTCAATGGAGATACCTCACTTTTAAATGCCCGGAGCGCTTTAGAGTGT	287
QY	939	GGGACAGAAAGGCNAATCACATGCCCAAAAGATATACCAATAGTTCGGCTTAAGAACCAAGCGT	998
Db	288	GGGGAGAGAGTTTACCTGTCACACAGAACATAGAGTGTCTGGCAACAAAGCCAGCTG	347
QY	999	CGTGTCTCTGCTCTTTCACTTACACAGCCCGTCTGGGGTTGTCTGTCTCCCACTA	1058
Db	348	TGTATTTTCATGTTTCTTTCATCTTACGGCATTCACTGTGGATTTATTTGTCAACCAATTA	407
QY	1059	CCCAAGAGACTATGGCAACCACTCCATGCTGTCTGGCTCATCTCGGCGAAGCCGAGAG	1118
Db	408	TCCAGAGAAATATGGAAACACATGAACTGTCTGTGTTGATTACTGGAGCCAGAG	467
QY	1119	CCGATCCACCTTGCCCTTCAACGACATTGACGTGAGGCTCAGTTTGAATTTCTGTGAT	1178
Db	468	TGGAATTCACCTTAATCTTTAATGATTTGATGTGAGCTCAATTTGACTTTCTGCGGT	527
QY	1179	CAAGATAGGGGACACCGCCGAGAGCCCGTCTGGGACCTTTCTAGAGAAACAGCTTC	1238
Db	528	CAAGATATAGGCAATTTCTGACATTAACGTCTGGTACTTTTCTTGGCAATGAGTGCC	587
QY	1239	CTCTCTCATCAACAACAGTGGCCACGTGAGCCCGTCTCAGTTTCCAGATCCCACTCCAC	1298
Db	588	TTCCAGGCTGGCAGACAGTGGGCATATAGTTGCTTGGAAATTTCACTGTGACATTCAC	647
QY	1299	AGGGAAGAGGGCTTCAACATCATCTTTTACCACTTTCCGACAAACGAGTCCCGGATCC	1358
Db	648	TACTGGCAGAGGGTTCAACATCACTTACCAACCAATTTGGTGAATGAGTCCATGATCC	707
QY	1359	TGGCGTTCCAGTAATATGGCAACGGTTTGGGGACAGCTCCAGCTGGGACGTCATCTC	1418
Db	708	TGGCATTTCTTAATTAACGAGCAAGCTTTTGTGACAGGTTTCTACTCGGAGCTGGTTTC	767
QY	1419	CTTCTCTGTGATGGAAGCTTCTTGGGACTCAGGGCTCAAGAACATCACTGCGTCTCT	1478
Db	768	TTTCACATGTGATGATGGCTTTGTCAAGACCAGGGATCCGAGTCAATTCCTGATACT	827
QY	1479	GAAAGAGGGCAGCGTGTCTGGAACAGCGCTGTGTGGGTGTGAAGTCCCTGTGTGG	1538
Db	828	GMAAACGGGAACGTGTGTGAGGCTCCACCGTGGCCGTGTGAAGCTTCATGTGTGG	887
QY	1539	TCACCTGACTTGGCCAGCGGACCATCTCTCTCGGGCTGGCCCTGTCTTCAAGGA	1598
Db	888	ACATGTGACAGGCTCAGGGAGATTTTGTCTCTGTGATGGCCAGGATTTATTAAGA	947
QY	1599	TGCTTGAAGCTGTGCTTGGTGAATGAGGCCACGCGAGCTAACCCCATCAAAATCACCTT	1658
Db	948	TTCTTTACATGTGTGATGATTAATTAAGCAAAACAGGCCCACTTACAAATAACTTT	1007
QY	1659	CGACGATTTCAAAACCGAAGTCAATATGACACCTGTGAAGTGAAGCAATGGGCGGACTTA	1718
Db	1008	TGACGATTTTCAAGACAGAGTCAATTAATGACACTTTGAGAGTCAGAGATGGGACGAC	1067
QY	1719	CTCAGCGCCCTTGTAGCGGGTTTACACAGGGAACCCAGGTTCCCAAGTTCTCATCAGAC	1778
Db	1068	TTCTGCTCCCACTGATTCGGGAGATACACGCGACCCAGGACCCCAAGTTCTCATCAGAC	1127
QY	1779	CAGCAACTAACCTTACCTTCTTCTTCTTACCGACAAAGTCACTTGGACATCGGCTTCA	1838
Db	1128	CGGGAATTCATGATCCTGTCTATTACCACTGACAAACGCGCTCAGACATCGGCTTCT	1187
QY	1839	GCTCCGCTATGACTATTAACACTGCAGTCAAGACATCTGTGATCCAGGAATCCCACT	1898
Db	1188	CATCACTATGAGATGTGAGCGCTTGAATCGGATTTCTGTCTGACCCGGGCAATCCGT	1247
QY	1899	AAATGACAGGCTCATGGGAATGACTTTCACTGTGGGCGCGCTGTGACTTTACGCTTGA	1958
Db	1248	GAACRCATGCCACGGTGAAGCTTTGGATCAAGTTCACAGTGAACCTTTACGCTTGA	1307

QY	1959	TCGGGGCTACACATTAAAGTGAAGGGAGGCGCTGAGAGTGAGGCCCAACTTCAGTGGAG	2018
4Db	1308	CCGGGGGTACACACTAAAGTGAAGAGCGCCCTGCTGTGTAGAGGAACCAACAGTGGAA	1367
QY	2019	CCGGGCGCTGCGCCAGTTGTGTGAAGCTCTCTGTGTGTGGCTTCAATTCAGAGCTTCAGTGGAC	2078
Db	1368	CCAGCGCTTGGCCGAGCTGCGAGCGCTTAATGTGAGGGCTACATCCAGAGGAAGTGGAAC	1427
QY	2079	CATCTTGTGCGCAGGGTTCCTGTACCTTCACCCCAACAATTGAATTGCAACTGGATTTAT	2138
Db	1428	AGTCTTTCTCTGGGTTTTCCAGATTTTTTAACAACTCTTAAACVGCAGCGTGGACAT	1487
QY	2139	CGAAACAATCTCATGTGGCAAGGGTGTCTTCTACTTTCCACACTTCCACTGGAAAGTGG	2198
Db	1488	TGAATGTCTCATGTGGAAAGGATTCAAATGATCTTTCACACCTTTTCATCTTGAGATTC	1547
QY	2199	CCATGACTACCTCCTCATCATGGAAGAGGAGCTTACACCAGCGCCCTGAGGGCGCTTAAC	2258
Db	1548	CCAGGACTATTACTGATCACAAGAGATGGAAGTTTTTCCGAGGCCGTTGCGCAGGCTCAC	1607
QY	2259	TGGATCTTGGGTGCGCAAGCTCCCATCAGCGCTGAGGCTCTATAGCAACTTCACTGCGCAGT	2318
Db	1608	CGGGTCGGTGTGTGCTCTACATGATCAAGAGGAGCGCTGTTTGGAAACTTCACTGCGCAGCT	1667
QY	2319	CCGCTTACCTCTGATTTTCTCAGTGCATATGAAGATTCAAACTCATTCTCAGAGTA	2378
Db	1668	TCGGTTTTATTCAGACTTCTCTCAATTTGTATGAGAGGGCTTCAMATATCAATTTTCAGATA	1727
QY	2379	CGACTTGAAGCCCTGTGAGGAGCGCCGAGGTCACAGCTCAAGCATTCGGAAGGGCTTGCA	2438
Db	1728	TGACTTGAAGCATGTGATGATCTTGAAGTCCCTGCTTCAAGCCGAAGAAATGGTTTTTCA	1787
QY	2439	GTTTGGCGTGGGCGACACCTTGACCTTCTCTGCTTCCCGGAGTACCGTGTGAGGCGAC	2498
Db	1788	CTTTGGTGTGGAGAGCTCTGAGATTTTCTGCTTCTGTGGATATGTTTAAGAGGTGC	1847
QY	2499	CGCCCGCATCAGTGCCTGGGGGGCAGACGCGCCTGTGAGCTCGCTTCTGCCAAGTG	2558
Db	1848	CRCCAAAGCTTACCTGCGCTGGGTGGGGGCGCGCTGTGTGAGTGCACCTCTGCCAAGTG	1907
QY	2559	TGTTGCTGAGTGTGGGAATTCAGTCAAGAGACTCAGGGTACTTGTGTCTCCCAACTT	2618
Db	1908	TGTGGCCGAATGTGAGCAAGTGTCAAGGAAGGAAGAACTTACTGTCTCCAAATTT	1967
QY	2619	TCTGTGAACTACATATAATCAATCATGTGATGATTTCTCATCTCAGACCCAGCCAGGAA	2678
Db	1968	TCATATCCATTATATATATAATACATGATGTATTTATAAATGAAACAGAGCGGCAC	2027
QY	2679	GGGAATTCAGTGAAGAGCGAGGACTTGAACTCTCCGAAGAGATGTCTCAAGTTTA	2738
Db	2028	GGGCACTCACCTTAGAACAAGAACTTCCAGCTGTTTGAAGGAGATCTCTAAAGGTATA	2087
QY	2739	TGATGGCAACAACAATCCGCGCGTTTGTGTGGAGTTTTTAAGCATTTCTGAGATGATGG	2798
4Db	2088	TGATGGAAGAAAGAGTTCTTCACGTCCACGTGGGACGTTCACTAAATATGAATCTTGTGG	2147
QY	2799	GGTGACTTTTGAACAGCAATCCAGACGTCGTGGCTTGATTTTCATCTAGTGTCTGAAAA	2858
Db	2148	GCTGATCTTAACAGCAATCCATCACTCTGTGCTAGATTTCAACACCAATGATGTGA	2207
QY	2859	CACGAGCAAGGGCTTTGAATGCACTTTTCCAGCTTTGAATCAATCAATGTGAGAGCC	2918
Db	2208	CACGAGCCAAAGTTTTTCAACTCACCTATACAGATTTTGAATCTGGTAAATGTGAGATCC	2267
QY	2919	AGGAACCCCAAGTTTGGCTTACAAGGTTCAATGATGAAGGTTCATTTTGCAGAGAGCTCCGT	2978
Db	2268	GGGCACTCCCTAATCAACGCTATATAGATTCGATGAAGGCGCACTTTACCAACACTGATGT	2327
QY	2979	GTCCTTACGCTGTGACCTGTGATACAGCTGTGCGGGGTGATGAGAGAGTGTCTGTGTGAG	3038
Db	2328	TCTGTACAGTTTGAACCCGGGGTACGCGCATGTGATGAGCAACACCTGTACTGTTTTGAG	2387
QY	3039	TGAGAGGCGCGAGCTTGGAGCTCGGCGCTTCCCACTGTGTGCGCGAGATGTGAGAGGAC	3098

Db 2388 TGGAGACAGGAGAGTGTGGAGCAAAACCACTTCTGTGCTAGTGGGATGTGGTGTCA 2447  
 Qy 3099 AGTGAAGAGAGAGTGTGGGAGAGTGTGTCAACCCGGATATCCAGCTCCCTATGAA CA 3158  
 Db 2448 GATTCATGAGGACATATGAGAGCAATATGTCTCCCTGGCTATCCAGCTCCGATGAA CA 2507  
 Qy 3159 CAATCTCACTGATCTGTGACATATGAAAGCAAGGCGGCTGACACATTTGGCTACATT 3218  
 Db 2508 CAACCTCACTGACCTGTGATTAATAGAGGCAACCGAGAAAGACCATTAAGCTTCATTT 2567  
 Qy 3219 CTTGGTGTGACAGAGAGAGTTCACGACGTGTGCGCATCTGGATTTGGGCTGTGGA 3278  
 Db 2568 CATTTGTTTTCAGACAGGAGATGTCTACGACATCTCAAGGTCTGGAGCGGCGGTGGA 2627  
 Qy 3279 GAGCGGGGTTCTGTGAAGAGCTGAGTGGCCGGCGCTGCAAGACCTGATATGAC 3338  
 Db 2628 CAGTGAATCTGTGGAAGAGTGGAGTGGCTCCGCCCTTCCGAGGACATTCACAGCAC 2687  
 Qy 3339 CTTCAATGTGTGTCTGTGACATTTGACATCTGATTTTTCACAGACAGGCTTTGC 3398  
 Db 2688 CTTCAACTCTACCTGACCTGTGAGTGTGACAGGACCTTTTCATGACAGTCTGCTTCTC 2747  
 Qy 3399 CATTCATTTTCAAGTGTCCACAGCAACGTCTGCAATGACCTGGGATCCCGAGAAATG 3458  
 Db 2748 CATTCAGTTCTCACTCAATTTGCAAGCCACTGTAAAGATCCAGGATGCCCCAATAATG 2807  
 Qy 3459 GAGTGGAGTGTGTGACATTTGGAGACCGGCGCATTCACAGTGTTCAGTGTGACCTTGG 3518  
 Db 2808 CACCGGCTATGAGAGACAGAGAGGCTGGAAGACCGTCACTTCAGATGTGACCTTGG 2867  
 Qy 3519 CTAACGGCTGTGAGGAGAGTGCAGATGAGTGTGTGAAGATCGAAGACAGTCTTGG 3578  
 Db 2868 CTATCAGCTTCCAGAGCAAGCAAAATCTGTGTGACGTGAATTAACGGTCTTTTG 2927  
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 Db 2928 GCAACAGACCTCTCTATGATGATGATGCTGTGTGAGGAATCTGACGGCGCCAGCAGG 2987  
 Qy 3639 AGTCACTCTCTCAACAAATTAACCGAACCTTAACCGCGCAGGAGAGATGTGACTGGA 3698  
 Db 2988 TGTATTTTGTGACCCCACTACCCAGCGGATCTCTCTGGAGAGGATGTGACTGAG 3047  
 Qy 3699 AGTGAACGCTCAACGAGCTAGGTGATGCGCCGATTTAAATCTTTAACTTGAAGC 3758  
 Db 3048 AGTAAAGTGAACCGGAGCTTTGTCTATGCGCTGTGATTAATCAAAAGTTTAAATGAGCC 3107  
 Qy 3759 TGGCTATGACTTCTCTCATATCTACGACGAGCGGACTCTCTAGCCCTCTCATAGGA 3818  
 Db 3108 CAGCTATGACTTCTCTACATCTATGAGGGGAAATTCACAAGCCCTCATTTGGAG 3167  
 Qy 3819 CTTCTATGTGCTCCAGCTCCGAGCGGCTTGAAGACAGACAGACAGCTCTTCTGCG 3878  
 Db 3168 TTAACAGGGCTCTCAGGCGCCCAAGAAATAGAGATGACGGAACAGCTTCTTGTGCG 3227  
 Qy 3879 CTTCCGAGAGATGATCTGTGAGCAATGTGGCTCTGCTCATTTGATATAGAAAACCC 3938  
 Db 3228 ATTTGGAGTGTCTCTCGTGCGCTTTTCAAGGTTCCGCTTTGAATTTAAAGAAAC 3287  
 Qy 3939 GCGGAGTCAATGTTTGTGATCTGTGCTCATCAAGAACGAGCAACGCGGTGGCTCGACCT 3998  
 Db 3288 AGGGAAGCTTGTGTTGACCCAGGAATTAATGAATGGAACAAAGTTGGAACAGACTT 3347  
 Qy 3999 GAAGCTGGGCTCTCCGTCACTTAATGCGACGCGGGCTAGAGAGTTGAGAGGACCTTC 4058  
 Db 3348 CAAGCTTGTGCTTCAACATCACTTAACAGTGTGCTGTGCTTAATTAATTTTGAACCTTC 3407  
 Qy 4059 GACCTGAGCTGATCTCTGGGCGCTGATGGAGAGCCGTGTGGAACAATCCCGGCACT 4118  
 Db 3408 ATTCATCACTGTGTGATTTGGGCTATGGGAAACCTCTCTGGGACCAAGTGTGCTTC 3467  
 Qy 4119 CTGACAGCCCTGTGTGGGAGACGATGTGGTTCGACGAGTGTCTTGTCCCA 4178

Db 3468 CTGCAATGTCTCTGTGTGAGGACGATACAGGGATCAGAAAGGGATTTATCACCAA 3527  
 Qy 4179 CTACCCCAAGATCAACACAGTGAAGATCTGTGTATTTTGTATCTGCCCCAAGA 4238  
 Db 3528 CTACCCCAATTAATCAACAGTGTCAAAATGTCTTATTCATCAACGATCCAAAGA 3587  
 Qy 4239 CTATGTGTGTGTGGCAGTTTGGCTTTTCAACAGGCGCTCAACAGCTGTGTGAGT 4298  
 Db 3588 ATTTGTGTCTTTGAGACAGTTTGTCTATTTTCAGACAGCCCTGATATGATTTGGAGATT 3647  
 Qy 4299 TCACAGCGGCAACAGCAGACATCTGGCGCTCTCAAGTCTCTCTCGGCTCCATACAG 4358  
 Db 3648 ATTTGATGAACCATCAGACAGGCAAGCTTCTCACTCTCGGGGTCTCACTAGG 3707  
 Qy 4359 AGAATCACTGCGCTTGGCCACTCCATCAAGTTCTCAATTAAGTTAGCGCCAAAGCCT 4418  
 Db 3708 GGAACATGTGCTTGTGCTAGTCAATCAAAATCTCTCGAATTCAGTGCAGAGACCG 3767  
 Qy 4419 CGCACAGCAGAGGCTTCACTTTGTCTACCAAGCGGTTCTTGAAACAGCGCCAGCA 4478  
 Db 3768 TGCCTGTGCGCGGCTTCCATCTGTATCAAGCTGTCTGTACAGTGAACCA 3827  
 Qy 4479 GTGCACTCTGTGCGGAACCCGCTATGCAAGAGGCTGGGACATCTTCTGGTGG 4538  
 Db 3828 ATGCAAGCTGTCTCCGAGCCAGATACGAAAGAGATGTCTGAGTTTCTGCGG 3887  
 Qy 4539 GGCATGTGCGCTTCAATGCAACTCGGCTATGCCCTGAGGGGTGCGCAGATGCA 4598  
 Db 3888 CTCATGTGCTGATTCAGTTCACAGCCGGAATCTCTGTTCAAGGTTCAAGCGGCTCA 3947  
 Qy 4599 GTGCTCTCTGTGCTGTGGGCTTGGCCCAATGGAATGTCTCAGCGCCACGTGTGTGT 4658  
 Db 3948 CTGCGAGTCGCTGCGCAACGCTTGGCAGATGGAACAGATCCCAAGCTGTGTGT 4007  
 Qy 4659 GCGGTGTGAGGCACTCTACAGAGCGGAGGAGCAATCTGTCTCCCTGGCTTCCAGA 4718  
 Db 4008 ACCCTGCAAGTGCATTTCACTCAAGAGAGTCAATCTGTCTCCCGCTACCTGCA 4067  
 Qy 4719 GCGGACTCTCAACAGCCTCAACTGTGTGTGAAGATGTGTGCTCCGAAAGCGCTGAGAT 4778  
 Db 4068 GCGATAGGAAACAATTTGAATCTATATGGAATATATGTAAGAGGCTGGGAAT 4127  
 Qy 4779 CCAAGTCAAGTTGTCAAGTTTGTGACAGACAGAACTGGACTGTGCTGGAATTTGA 4838  
 Db 4128 TCAGATCCAAGTATCAAGTTTTCACAGAGCAAACTGGGACTCTCTTGATGATCAAGA 4187  
 Qy 4839 TGTGTGAGATTAACCTGTAACAGATGCTGGGAGTTTCTCAGGAACAACCGGCGCT 4898  
 Db 4188 TGTGTGGATGTGACCGACCCAGACTGGGAAGCTTCTCAGGACACACAGTACGGCACT 4247  
 Qy 4899 TCTGAACGACACTCAACAGCTCTACCTTCAATTTCTACTCAGATATCAGCTATGCG 4958  
 Db 4248 GCTGAACGATCTTCCAAACCAACTCTACCTGCAATTTCCAGCTGACATTAATGTGGCAGC 4307  
 Qy 4959 AGCTGGCTTCACTTGAAGTCAAAACGCTGGGCTGAGCAAGTTGTCCGAACTGTCTGT 5018  
 Db 4308 TGTGTGTTTCACTGGAATCAAAACGTGTGCTGTCTGCTCAAGCCAAAGAACAGCCCT 4367  
 Qy 5019 GCCCAATACCGGGTGAAGACTGCGAGCGCTACTCTGTGATATGATGTGTGCTTTTCA 5078  
 Db 4368 CCCCAAGCAACAGATCAAAATCGAGATCGGATACGTGTGAACAGCGTCTCTCTTCA 4427  
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QY 5259 CTCCTGGAAATAGCATGCGCGTGGGCTTTGGAGTCACATCCAGTTCGTGAACCTTTC 5318  
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| | | | |  
QY 5439 CACCGGTATTTCCACAGGACCACTCCCAATCGGCCAGATTCAGGTGAGATATCA 5498  
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Db 4788 CCTCATTCACCTTTATATGATACATTCGCAAAACCGGCAAGATTTAAATTTCTTACCA 4847  
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QY 5739 GGGGTTCCCTAGCCGCTACTCCAGCTCCAGACTGTGTGCTGATCACCGTGCAT 5798  
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Db 5148 AGGGACGAGATTTACATCACTTCACTTCAAGAGCGAAGCTGTCAACATTAACAT 5207  
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QY 5859 CACCATCTGGAGTGGCCACAGCAACAGACCAAGCGCTGGCTTCCACCCGAGCAT 5918  
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| | | | |  
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| | | | |  
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| | | | |  
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| | | | |  
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QY 6339 CCTCAGTGGAGTACTTCTCTGAGGAGCAATATGATGATGATTTGATGAG 6398  
| | | | |  
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| | | | |  
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| | | | |  
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| | | | |  
QY 6579 TGGCTTATCTTAGGCAAGACAGACCAAGCCCGGGGCTCCATCACTTTGGCTGCA 6638  
| | | | |  
Db 5928 TGGGGGTATTTTAAACAGACTGACAGAGCGGTGGAAGCAAAAGTGCATTTATTTGCA 5987  
| | | | |  
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| | | | |  
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| | | | |  
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| | | | |  
Db 6708 CACGGTGTATTAACAGTGAATCTGTGTGCTGTGTGGGAACTTCCGTGTGAGGATATG 6767  
| | | | |  
QY 7419 CCAAGCAGATTCATCTGATCGGGCAAGACCCCTTTCTGTGTGCCAATTAACGTGTGACA 7478  
| | | | |

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Db      6768  CCTGCAAGATCCAAAGTGTCTGAGCAAAACGCTTCTGTGTCCCATCATATGTGGCA 6827
Qy      7479  CCCAGCAACCCCTGTCAACGCGCTCACTCAGGGTAACAGTTTAACTTCAACGATGTGGT 7538
Db      6828  CCTGTGAAACCTGCGCCACGAGTATCACTAATGGCAGTGAATTCAACCTGAATGATGTGT 6887
Qy      7539  CAAGTTTGTGGCAACCTGGGTATATGGCTGAGGGGGCTGTAGTGTCCCAATGCTTGGC 7598
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Qy      8439  AATATGCTGTGCTCCGCTATATATGATGATGACATATAGATATCTGTGTGAGCTGCAC 8498
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RESULT 15  
 AAD33318 standard; cDNA; 10673 BP.  
 ID AAD33318; standard; cDNA; 10673 BP.  
 AC AAD33318; standard; cDNA; 10673 BP.  
 XX  
 DT 01-JUL-2002 (first entry)  
 DE Human C3b/C4b complement receptor like cDNA #1.  
 XX  
 KM Human; C3b/C4b complement receptor-like molecule; immune system disorder;  
 KM gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis;  
 KM inflammatory arthritis; inflammatory joint disease; Alzheimer's disease;  
 KM multiple sclerosis; inflammatory bowel disease; nervous system disorder;  
 KM transplant rejection; autoimmune disease; ischaemic condition; neotropic;  
 KM metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus;  
 KM infertility; vasodilator; obesity; cardiac; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 FT CDS 334..9543  
 FT /tag= a  
 FT /product= "Human C3b/C4b complement receptor like protein  
 FT #1"  
 FT /transl\_except= (pos:2416..2418, aa:Xaa)  
 FT /note= "This translational exception occurs while  
 FT decoding the alternative version of human C3b/C4b  
 FT complement receptor like protein #1 (AAE20900)."  
 XX  
 PN MO200210199-A2.  
 XX  
 PD 07-FEB-2002.  
 PF 24-JUL-2001; 2001MO-US023232.  
 PR 02-APR-2000; 2000US-0222504P.  
 PR 28-NOV-2000; 2000US-00728787.  
 XX  
 PA (AMGB-) AMGEN INC.  
 XX  
 PI Melcher AA, Elliott GS;  
 XX  
 DR WPI; 2002-303934/34.  
 DR P-PSDB; AAE20787, AAE20900.  
 XX  
 PT Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic

PT acid molecule, useful for treating, preventing and diagnosing rheumatoid  
 PT arthritis, psoriatic arthritis, inflammatory arthritis, and multiple  
 PT sclerosis.  
 XX  
 PS Claim 1; Fig 1; 251pp; English.  
 XX  
 CC The invention relates to a nucleic acid encoding a novel C3b/C4b  
 CC complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like  
 CC polypeptide and nucleic acid molecules may be used to treat, prevent,  
 CC ameliorate, diagnose and/or detect diseases such as immune system  
 CC disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory  
 CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune  
 CC disease, multiple sclerosis, lupus, inflammatory bowel disease,  
 CC transplant rejection, nervous system disorders (e.g. Alzheimer's  
 CC disease), ischemic conditions, metabolic disorders (e.g. obesity and  
 CC diabetes) and infertility. The invention is useful in gene therapy. The  
 CC present sequence is human C3b/C4b complement receptor like cDNA  
 XX  
 SQ Sequence 10673 BP; 2690 A; 2711 C; 2574 G; 2691 T; 0 U; 7 Other;

Query Match 40.1%; Score 4067.4; DB 6; Length 10673;  
 Best Local Similarity 65.5%; Pred. No. 0;  
 Matches 6001; Conservative 5; Mismatches 3136; Indels 25; Gaps 3;

QY 819 AGAGATCGAGCAGGCGAGTTGCGGTGACCTGCGCATACCTGATATGCGCGGAGG 878  
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 DB 468 CAGCAGTTTCTTCATGAGATGATCACTACCTTTGAATGCCGCGGCTTTGAGCTGT 527  
 QY 939 GGGACGAAGGCAATATATCCCAAAAGATTAACATATGTCGCTAAGAGCAGCTG 998  
 DB 528 GGGGAGAGATATATCACTGTGACGAACATATGATGTCGGAACAGGCCAGCTG 587  
 QY 999 CGTGTCTCTGCTTCTTCACTTCAACGAGCCGCTGCGGAGTGTCTGTCTCCAACTA 1058  
 DB 588 TGTATTTTATGTTTCTTCACTTCAACGAGCTATCTGAGATTTATCTGTACCAATTA 647  
 QY 1059 CCCAGAGACTATGGAACACCTCCACTGTGTGTGCTATCTTCTGAGGAGGCTGAG 1118  
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 QY 1119 CCGCATCACTGCGCTTCAACAGCAATGATGAGCTCAAGTTGATTTCTGTCTAT 1178  
 DB 708 TCGAATTTCACTTATATCTTATATGATTTGATGAGCTCAATTTGACTTCTCGCGGT 767  
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 DB 888 TACTGCGAGAGGGTTCAACATCACTTACACCATTTGTGAGAAATGAGGCGCATATCC 947  
 QY 1359 TGGCGTTCCAGTAAATGGAACAGGTTTGGGGGACGCTTCAGCTGGGAGGCTTCATTC 1418  
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 QY 1539 TCACTGACTTGGCCAGGCGGACCATCTCTCTCGGGGTGGCTTGTCAAGAG 1598

Db 1128 ACATCTGACGCTGCAGGAGGTCAATTTGCTCTGATGGCCAGATATTATAGGA 1187  
 Qy 1599 TGCCTTGAAGTGTGCTGGGTGATGAGGCCAGCCAGGCTACCCCATCAAAATCACCTT 1658  
 Db 1188 TTCTTTAATGTTGATGATGATTAATGAGCAAAACAGGGCCACTCTATCAAAATATACCTT 1247  
 Qy 1659 CGACAGATTCAAAACCGAGGTCACTATGACACCTTGAAGTACCCGATGGCGGACCTTA 1718  
 Db 1248 TGACAGATTTCAGACAGAGGTCAATTAATGACCTTGGAGGTCAAGATGGCGCAGCAG 1307  
 Qy 1719 CTCAGGCGCTTGTATCGGGGTTTAAACAGGGAGCCAGGTTCCCACTTCTCATCAGAC 1778  
 Db 1308 TTTCGCCCACTGATGGGAGTACACGGGACCCAGGACCCCACTTCTCATCAGAC 1367  
 Qy 1779 CAGCAACTACCTTCTACCTCTCTCTTAACGACAGAGTCACTGGACATCGGCTTCA 1838  
 Db 1368 CGGGAACCTTCATGTACTGTCTATTCACTGACAAAGCCGCTCAGGATCGGCTTCT 1427  
 Qy 1839 GCTCGGCTATGAGCTATAACACTGACGACCACTGTCTGATCCAGAAATCCCACT 1898  
 Db 1428 CATCACTATGAGAGTGAACGCTTGAAGTTCCTGCTGACCGGCGATCCCTGT 1487  
 Qy 1899 AATAGACAGCGCTATGGGATGACTTCTACGTTGGCGCGCTGGTGAACCTTCACTGTA 1958  
 Db 1488 GAACGRCATTCGCAAGGTGAGACTTTGGCATCAGTCCACAGTGACTTTCACTGTA 1547  
 Qy 1959 CTCGGGCTACACATTAAAGTACGGGAGCCTCTGAGTGTGAGCCCACTTCACTGTA 2018  
 Db 1548 CCCGGGGTACACACTTAAGTGAAGAGCGGCCCTCGCTGTGAGAGAAACCACTGTA 1607  
 Qy 2019 CCGGGCCCTGCGCACTTGTGAGCTCTGTGTGGCTTCACTTCAAGCTCAGTGGAG 2078  
 Db 1608 CCAAGCTTGGCCAGTGTGAGCTCTATGTGAGCTACATCCAAAGGAAAGTGTGAA 1667  
 Qy 2079 CATCTTGTGCGAGGCTTCCCTGACTTCTTACCCCAACACTTGAACCTGATTAAT 2138  
 Db 1668 AGCTCTTCTCTGGGTTCCAGATTTTATCCAACTCTTAAACATGACGTGACAT 1727  
 Qy 2139 CGAAACATCTCATGCGAGGAGTGTCTTCACTTTCCACACTTCCACTTGAAGTGTG 2198  
 Db 1728 TGAAGTGTCTATGAGGAAAGAGTTCMAATGATCTTTCACACCTTTCATTTGAAGTTC 1787  
 Qy 2199 CCAATGCTACCTCTCATCTGAGAGAGCGAGCTTCAACGAGCCCTGAGGAGCTAAC 2258  
 Db 1788 CCAAGCTATTTAATCTATCAAGAGATGAAATTTTCCAGACCCGTTGCCAGGCTCAC 1847  
 Qy 2259 TGGATCTCGGCTGCGAGCTCCCATCAAGCGCTGGGCTCTATGGCACTTCACTGCGCAG 2318  
 Db 1848 CGGGTGGGTTGCTCATACATCAAGGAGGCTGTTGGAACTTCACTGCGCAGCT 1907  
 Qy 2319 CGGCTTCACTCTGATTTTCTCCATGTCATATGAAGATTCACATCACTTCTCAGAGTA 2378  
 Db 1908 TCGGTTTAATCAAGACTTCTCAATTCGTAACGAGGCTTCAATATCAATTTTCAAAATA 1967  
 Qy 2379 CGACTTGAAGCCCTGTGAGAGCGGAGGCTCCAGGCTACAGCATCCGGAAGGCTTGA 2438  
 Db 1968 TGACTTGAAGCCATGTATGATCTTGAAGTCTTCTGCTTCAAGGAAATGTGTTTGA 2027  
 Qy 2439 GTTGGAGTGGGAGACCTTGAACCTTCTCTGCTTCCCGGCTACCGTCTGAGGGCAC 2498  
 Db 2028 CTTTGGGTGGAGACTCTCTGAGCTTTCTGCTTCTGAGATATGTTTGAAGAGTGC 2087  
 Qy 2499 CGCCCGCATCAGTGTCTGGGGGGCAGAGCGGCGCTGTGAGTCCGCTTCTGCAAGTG 2558  
 Db 2088 CIRCACAGCTTACCTGCTGGGTGGGGCCGCGTGTGTGAGTGAACCTTGTGCAAGGTG 2147  
 Qy 2559 TGTGTGAGTGTGGGAATTCAGTCAAGGCACTCAGGGTACTTGTCTGCCCCCACTT 2618  
 Db 2148 TGTGGCCGATGTGTGAGCAAGTGTCAAGGAATGAAGAACTTACTGTCTCAAAATTT 2207  
 Qy 2619 TCTGTGAACATAATTAACATCATGATCATCTCATCCAGACCCAGCGAGGA 2678

Db 2208 TCCATCCATTATGATATATAACCATGATGTATCTATTAATAATAGAAAACAGAGCCGCA 2267  
 Qy 2679 GGGAAATTCAGCTGAAGCCAGGGCATTCGAACCTCCGAAGGAGTCTCTCAAGTTTA 2738  
 Db 2268 GGGGATCCACTTAAGAACAGAACTTCCAGCTGTGTGAAGAGATCTCTAAAGGTATA 2327  
 Qy 2739 TGATGCAACAACTCCGCGCTTGTGAGGAGTGTGTGAGGCTTGTGAGATGTAGG 2798  
 Db 2328 TGATGAAAAGACATGCTTCTCAGCTCAGGACAGTTCATTAATAATGAATCTTGGG 2387  
 Qy 2799 GGTGACTTTGAACAGCATTCAGACAGTCTGTGCTGATTTCACTATCTGCTGAAA 2858  
 Db 2388 GCTATCTTAAACAGCATTCATCACTCTGTGCTATGAGTCAACCAATGATCTGA 2447  
 Qy 2859 CACGAGAAAGGCTTGAACGTGCACTTTCCAGTTTGAATCTCAATATGTAGAGCC 2918  
 Db 2448 CACGACCAAGTTTCACTACCTATACCGATTTGATCTGTAAATGTAGAGATCC 2507  
 Qy 2919 AGAACCCTCAAGTTTGGCTAACAGGTTCAAGATGATGATTTTTCAGGGAGCTTCGT 2978  
 Db 2508 GGGCATCCCTTAACATAGGCTATAGGATCCGTATGAAGGCACTTACGACACTGTAGT 2567  
 Qy 2979 GTCTTGAAGTGTGACCTTGGATACAGCTTGGGGTATGAGAGAGTCTGTGTCTGAG 3038  
 Db 2568 TCTGTACAGTTGCAACCCGGGGTACGCTATGACATGACAGCAACCTGTACCTGTGTGAG 2627  
 Qy 3039 TGGAGAGGCGCGACCTGGGACCGGCGCTGCGCACTGTGTGCGAGTGTGAGGAGAC 3098  
 Db 2628 TGGAGACAGAGTGTGGGCAAACTTCTCTGTGCTATGACGAAATGTGTGATCA 2687  
 Qy 3099 AGTGAAGAGAGGTGTGCGGGAGTGTCTGTCAACCGGGTATCAGCTCTTATGAA 3158  
 Db 2688 GATCCATGACGCAATCAGGACGATATTTGTCCTCGGTATCAGACTCCGTATGACAA 2747  
 Qy 3159 CAATCTCACTGCACTGTGACATTCGAAGAGAGCCGGCTGACCAATTTGGGCTAACCTT 3218  
 Db 2748 CAACCTCACTGCACTGTGATTAAGAGGAGAGCCAGAAAGCAATTAAGCTTCACTT 2807  
 Qy 3219 CCTGGTGTGACACAGAGAGTTCACAGAGTCTGCTGCTGCTGCTGAGATGGGCTGTGGA 3278  
 Db 2808 CATGTTTTGACACGAGATGTGCTCAGACATCTCAAGTCTGTGAGCGGGCGGTGGA 2867  
 Qy 3279 GAGCGGGTGTGCTGAAGAGTGTGAGTGTGCGGCGCTGCGCAAGACTGTCAATGAC 3338  
 Db 2868 CAGTGAACATCTGCTGAAGAGTGTGAGTGTGCGGCTTCCGAGGACATTCACAGAC 2927  
 Qy 3339 CTTCACTGAGTGTGCTGCTGAGTTCAGACATGCTTCTTCAACGAGAGAGGCTTTCG 3398  
 Db 2928 CTTCAACTCACTCACTGAGTTCAGAGCTTCTTCAATCAAGAACTGTGCTGCTTC 2987  
 Qy 3399 CATCAATTTTCAATGTCACAGCAAGTCTGTCAATGACCCGTGAGATCCGAGAAATG 3458  
 Db 2988 CATCAAGTCTCACTCACTCAATTTGACAGCCACTGTATGATTCAGAGTATGCCCAAAATG 3047  
 Qy 3459 GAGTGAAGTGTGACAGTGTGGAAGCCGCGACTTCAAGATTTCCAGTGTGACCTTGG 3518  
 Db 3048 CACCGCTATGAGACAGCAAGAGGCTGTGAGACCTTCACTTCCAGTGTGACCTTGG 3107  
 Qy 3519 CTACCGGTGAGAGAGTGTGAGAGTGTGATGAGTGTGAGATTCGAGACAGATCTTCTG 3578  
 Db 3108 CTATCAGCTTCAAGAGCAAGCAAAATCACTGTGTGAGCTGTAAATACCGGTTCTTTC 3167  
 Qy 3579 GCAGCCAGCCCGCAATCATCTGCTTCTGCGGGGAGACCTTGAAGAGCAATCTGG 3638  
 Db 3168 GCAACCAACCTCTCTATGATGATGATGCTGTGTGTGAGGAGATGAGGGCCAGCAGG 3227  
 Qy 3639 AGTCACTCTTCAACCAATTAACCAAGACCTTACCCGAGGCAAGAGTGTGACTGAA 3698  
 Db 3228 TGTATTTTGTGACCACTACCACTACCAAGCCGTATCTCTGTGGAAGATGTGACTGAG 3287  
 Qy 3699 AGTGAAGCTTTCACAGACTAGCTAGCCCTGTATTTAACTTTAACTTGAAGCC 3758  
 Db 3288 AGTAAAGTGAACCGGAGCTTGTATCTGCTTGTATTTCAAAAGTTTCAACATGAGGCC 3347



QY	3759	GGCGATGATCTTCCCTCCCAATCTACGAGGACGGGACTCTCAGGCCCTCATATGAG	3818
Db	3348	CAGCTATATCTTCTACATATCTATGAAGGGGAGATTTCAACAGCCCCCTCATTTGGAG	3407
QY	3819	CTTCTATGGCTCCCGAGCTCCAGGCGCGATTTGAAGACGACAAAGCCTCTTCTCGC	3878
Db	3408	TTACACAGGGCTCTCAGGGCCCCAGAAAGATAGAGTACGGGAAACAGCCTGTTCTGGC	3467
QY	3879	CTTCCGACCGATGATCTGTGAGCAATGCTGGCTTGCTCATTTGACTATCAGAAAAACC	3928
Db	3468	ATTTCGGAGTATGCTCCGTGGGCTTTCAGGGGTTCCCAATTGAATTTAAAGGAAACC	3527
QY	3939	GGGGAGTCATGTTTGTATCTGTGTTCCATCAAGAACGGCACGGGGGGGGTCCGACCT	3998
Db	3528	ACGGGAACCTGTTTTGACCCAGGAATATATGATATGGACACAGAGTTGGAAACGACTT	3587
QY	3999	GAAGCTGGGCTCTCCGTCACTTACTACTGCCACGGGGGCTACGAAGTTGAGGGACCTC	4058
Db	3588	CAAGCTTGGCTTCACATCACTACCTACAGATGATGACTCTGGCTATTAAGATTTTTCAGCCCTC	3647
QY	4059	GACCCGTGAGCTGCACTCTGGGGCCGTGATGGGAAGCCCGTGTGGAAACATTCGCCGGCAGT	4118
Db	3648	ATCCATCACTGTGTGATTTGGGGCTGATGGGAAACCTCTCTGGGACCAAGTGTGCCTCTC	3707
QY	4119	CTGCACAGCCCCCTGTGGGGGACAGTATGTGGGTTCCGACGGAGTGTCTTGTCCCCCAA	4178
Db	3708	CTGCATATCTCCCTGTGGAGGCGAGTACACGGGATCAGAAAGGGATGTTTATCACCAA	3767
QY	4179	CTACCCCCAGAACTACACAGTGGACAGATCTGTTGTAATTTGTTACTGTGCCAAGGA	4238
Db	3768	CTACCCCATATTAACACAGCTGGTCAAAATATGCTCTATATTCATCAACGGTACCAAGGA	3827
QY	4239	CTATGTGTGTTTGGCGAGTTCCGCTTCTTTCACACGGCCCTCAACAGCGTGGAGGT	4298
Db	3828	ATTGCTGTCTTTTGGACAGTTTGCTTATTTCCAGACAGCCCTGATATGATTTGGCAGAAAT	3887
QY	4299	TCACGACGGCCACAGCAGCACTGGGGCTCCTGACGTCCTCTTGGGCTCCATACAG	4358
Db	3888	ATTGTATGAAACCCATGACAGGCGACAGCTTCTCAGCTCACTCTCGGGGTCTCACTCAGG	3947
QY	4359	AGAAATCATGCGCCTTGGCCACTCCCAATCAAGTTCTCATTAAGTTACGGCCAAAGCCT	4418
Db	3948	GGAAACATTTGCCCTTGGCTACGTCAAATCAAAATTTGCTCCGATTCAGTCAAGAAAGCGG	4007
QY	4419	CGCACACAGCCAGAGGCTTCACTTGTGTACCAAGCGGTTCTCTGAAACAGCGCCACGCA	4478
Db	4008	TGCTCTGCCCGGGCTTCACTTGTTGTATCAAGCTGTGTTCTGTACATGACACCA	4067
QY	4479	GTGCAGCTCTGTGCCGGAACCCCGCTATATGGCAAGGCTGGCAGTGACTTCTCGTGGG	4538
Db	4068	ATGCAGCTCTGTCCCCGAGCCCAAGTAACGAAAGGAATTTGTTCTGAGTTTCTGCCGG	4127
QY	4539	GGCCATCTGTCGCTTCAATGCAATTCGCGGATATGCCCTGACAGGGGTGGCCAGATATGA	4598
Db	4128	CTCATCTGTCGATTCAGATGACACCCGGGATACCTGTTCAAGGTTTCAAGCGGCTTCA	4187
QY	4599	GTGCTCTCTGTGCTGTGGGGCTTGGCCCAATGAAATGTCTACAGGCCCAAGTGTGTGT	4658
Db	4188	CTGCCAGTCCGGGCCCAACGCCCTTGGCACATGGAACACAGATCCCACTGTGTGTGT	4247
QY	4659	GCCGTGTGAGCAACCTCACAGAGCGGACACCATCTCTGTCCCTGGCTTCCAGA	4718
Db	4248	ACCTGTCACTGGAATTTCACTCAACGAAAGAGTCAATCTGTGCTCCCGGCTACCTCTGA	4307
QY	4719	GCCGTACCTCAACAGCCTCAACTGTGTGTGAAAGATCTGTGTCGCCGAAAGCGCTGGCAT	4778
Db	4308	GCCATACGGAAACAATCTGAATGTATATGAAAGATCATATTTACAGAGGGCTCGGAAT	4367
QY	4779	CCAGATCCAAAGTTGTCAAGTTTGTGACACAGACGACATCTGGGACTCGCTGGAAGTATTTGA	4838
Db	4368	TCAGATCCAAAGTACAGATTTTGTCCACGAGAGCAACTGGGACTCTCCCTGTGATTCACGA	4427

QY	4839	TGGTGCAGATTAACACTGTAAACCACTGCTGGGAGATTTCTCAGAGAACACCGGTGCTGGCTT	4839
Db	4428	TGGTGGGAGATGTAGACCGCAACCACTGGGAAGCTTCTCAGGACCAACAGTACCGGCACT	4487
QY	4899	TCTGAACAGCAACCTCCAAACGAGCTCTACCTTCAATTTCTCACTCAGATATCAGCGTATCTGC	4958
Db	4488	GCTGAACAGTACTTCCAAACCACTCTACCTGATTTCCAGTCTGACATTAATGTGTGGCAGC	4547
QY	4959	AGCTGGCTTCACTTGGAGTACAAACCGTGGGCGCTGACAGTTGTCCGAACTGCTGT	5018
Db	4548	TGCTGTGTTCCACCTGGAAATACAAAACTGTAGTCTTGCTGCATGCGCAAGAACGAGCCCT	4607
QY	5019	GCCCACTAACGGGGTGAAGACTGGCGAGCGCTACTTGTGTAAATATGTGTGTCTTTTCCA	5078
Db	4608	CCCCAGCAACAGCATCAAAATCGAGATCGGTACATGTGTGAACAGACGTCTCTCTTCCA	4667
QY	5079	GTTGTAGCGGGGATATGTGCTCTCCAGGGGCAAGCCCACTCTCTGCATGCGCCGGAACGT	5138
Db	4668	GTTCGAGCCCGGATACACCTTCGAGGGCGCTTCCACATTTTCTGTATGCCAGGACCGT	4722
QY	5139	GCGGCGATGAGAACTAACCTCTCTCCACTCTGTATTTCACAGTGTGGGGGAACAGTGAAGA	5198
Db	4728	TGCGCGTTGGAACATACTCCGTCTCCCTGTGATTTGACACGTGTGGAGGAGCGGTGAGAC	4788
QY	5199	GATGAGAGGGGTGATCTGTAGCCCCGGCTTCCAGGCACTAACCCAGTAACTATGACTG	5258
Db	4788	CTTGGGTGTGTGATCTTGAGCCCCGGCTTCCAGGTTCTTAACCCCAACTTAATGACTG	4847
QY	5259	CTCTCGGAAATATAGACTGCCCCGGGTGGGTGTGAGCTCACTATCCAGTTCCTGAACCTCTC	5318
Db	4848	CACCTGGAGATCTCATTAACCATCGGTATGTGACATATTAACATTTTCTGAAATTTTC	4907
QY	5319	CACCGAGCCCAACAGCACTACATAGAATTCGGAATGGCCCCCTATGAGACAGCCGAT	5378
Db	4908	TACGGAACCTATATCATGACTTCTTGAAATTCAAAATGGAACCTTAACACACAGGCCAT	4966
QY	5379	GATGGGAAGATTCAGTGGAGCGAGCTTCCAGCTCCTCTCTCCACGTCCACGAGAC	5438
Db	4968	GATTGGACAAATTTAGCGGCAACGGAATCTCCCGGGCCCTGCTGAGACAAAGCATGAAC	5027
QY	5439	CACCTGTATTTCACAGCGACCACTCCCAATTCGCGAGAGATTCAAGCTGGAGTATCA	5498
Db	5028	CCTATCCACTTTATATGTGACATTTGCAAAACCGGAGAGATTTAACTTGTCTTACCA	5087
QY	5499	GGCCATATGAATTCAGAGTGTCCAGACCCAGAGCCCTTTTCCATATGGCATTTGAGGGG	5558
Db	5088	AGCCTATATATTCAGAACTGTCCAGATCCACCCCATTTAGAAATGGGTACATGATCAA	5147
QY	5559	AGCTGGCTACAACTGGGACAATAGTAGACCTTGAGTGTCTCCGGGGATCAATTGAC	5618
Db	5148	CTCGGATTACAGCGTGGGCAATCGATATCTTTGAGAGTTATCTCGGGTACATTTAT	5207
QY	5619	TGGCCACCTTGTCTCAGGTGTCAACATGSCAACCAACCGAACTGGGACCAACCCCTGCC	5678
Db	5208	AGGCGATCTGTCTCCTCACTTGTACGCAAGGATCAACGAAACTGGAACTACCTTTTCC	5267
QY	5679	CAAGTGTAAAGCCCTTGTGGCGGGACATCACTTCTTCAACGGCACTGTGTACTCCC	5738
Db	5268	AAGATGTATAGTCCCTTGTGGGTACAACTTAATCTTCTGAACGGACCACTACTCCCC	5322
QY	5739	GGGGTTCCTTAGCCCGTACTCAGCTCCAGAGACTGTGTCTGGCTGATCACCGTGCAT	5798
Db	5328	TGGCTTTCCTGATGAGTATCCGATCTGAAAGACTGACTTTTGGCTCATCAGGTGCC	5387
QY	5799	TGGCCATGGCGTCCGCTCAACCTCAGCTGTCTGTGACAGAGCCCTCTGGAATTTTAT	5858
Db	5388	AGGGACACGAATTTACATCAACTTCAACCTCTTACAGCGGAACCTGTCAACGATTCAT	5447
QY	5859	CACCATCTGGATGGGCAACAGCAAAAGCAACAGCGTGGCGCTTCAACCCGAGAT	5918
Db	5448	TGCTGTTTGGGACGGTCCCGATCTCAAGACTCAACCCAGCTGGGAGTTTTCAGTGGCAACAC	5507
QY	5919	GGCCAGAAAAACGTGACAGAGTTTCACTCAACAGAGTCTGCTCAAGTTTCCACGTTAGTC	5978

Db	5508	AGCCCTGAAACCGCGTATAGCTCCACCAACCAAGTCTGTCTAAATTCCACAGGACCTT	5567
Qy	5979	AGCCACAGGGGGGATCTTGGCCATAGCTTTCTCCGCTTATCACTCACCAATGCCCCTCC	6038
Db	5568	TTCAAAATGAGAGCTTCTTTGTCTCAATTTCCAGCATTTTCAGCTCAAGAAATGTCMAAC	5627
Qy	6039	TCCCAACATCTCTCCCAACGCCCAAGCCGCACAGAAATGAAGATTAATATAGTGA	6098
Db	5628	TCCCCCAGCGGTTCCACAGGAGAAATGCTTACTGAGAGATGATGATTTTGAAGATAGANA	5687
Qy	6099	CATCGTACGCTACAGATGCTCTCCCTGGCTTTTACCTTAGTGGGGAATGAATTTGACTGG	6158
Db	5688	TTTGTGAAGTACAGATGCCACCCCGGGTACACTTGTGTGGGACCGCAATTTGACTTGG	5747
Qy	6159	CAAACTTGGAACTTACTGTGAGTTTGAAGACACCCCGCATATGTGAAGTGCACGTGCC	6218
Db	5748	CAACCTCAGTTCCCAAGTTGACGTTTGAAGGTTCTCTCCCAACATGTGAACACAAATGCC	5807
Qy	6219	AACAATGAGCTTCTGACAGACTCCACAGGCGGTATCCTGAGCAGAGCTAACCTGGAAG	6278
Db	5808	AGCAATGAAATCCGGAGCTGGATCATGGGAGTCATTCTCAGTCCAGGGATACGGGATAA	5867
Qy	6279	CTATCCCAAGTTCCAGACCTGCTCTTGGCTGTGAGAGTGAAGCCGACCTAATAACATCC	6338
Db	5868	TTATTTTAACTCCCAAGCTTGCTCTTGTGAAGTATTAAGTGAACCAACTCAACAACATAC	5927
Qy	6339	CCTCAAGTGGAGTACCTTCTCAGCAGAAAGCAATATGATGAGTTTGAATTTTGTATGG	6398
Db	5928	CATCTTTGTGACACATTTCAAATGAAAGCAATTTGATGCACTGGAAGTGTGTTATGG	5987
Qy	6399	TCCATCAGACAGAGTCTCTGTGCTGAAAGCCCTCAGTGGGAATTACTCAGCTCCCTGAT	6458
Db	5988	TTCTTCTGGGCAAAAGTCTCTGTGTAAGTCTTAAAGTGGAAATATATCTAACAATCAAA	6047
Qy	6459	TGTCAACCAAGCTCAAGCAACCTGTGTACCTGATCCTGATCATGATCAGCCCTAACATCG	6518
Db	6048	TTTTCACAAGCAGAGATATACATTTATATCTCCGCTGTCTCACTGACATGCCACAGTAA	6107
Qy	6519	GAAGGGCTTCAAGATCCGCTATTACGCCCTTACTGACGCTGCCAGGGCTCCACTCCA	6578
Db	6108	GAAAGATTTCAAAGATTCGCTATGACGACCTTACTGCAAGTTTGACCCACCCCTGAAAGA	6167
Qy	6579	TGGCTTCACTTAAGCCAGACCAAGACCCACCCGGGGGCTCCATCCACTTTGGCTSCAA	6638
Db	6168	TGGGGGTATCTTAAACAGAGACTGACAGAGCGGTTGAAAGCAAGTGAATTTATTTTGCA	6227
Qy	6639	CGCCGGCTAACCGCTGTGTGGGACACAGCATGGCCATCTGTAACCCGGCACCCCAAGGCTTA	6698
Db	6228	GGCTGGATACCGAATAGTGTGGGCAACAGAAATGCAACGTGTAGACGAACCACTTGGCAT	6287
Qy	6699	CCACTGTGAGCGAAAGCCATCTCTCTCTGTCAAGCTCTTTCCTGTGGGCTTCTCGTAGGC	6758
Db	6288	GTAACAAGTGGGACTCCCTCACGCCACTGTGCCAGGCTGTGTCTGTGAATCCAGAAATC	6347
Qy	6759	CCCAAGAAATGGAATGATGTTTGGGCAAGAGTACACACTGTGGAAACCAAGCCGCTGTACAG	6818
Db	6348	CCCAAGAAACGGTTCAATTAACGGGGAACGATTTCACTTTGACAGTAAAGTGTCTATGA	6407
Qy	6819	CTGCACTGAAGGCTAACACTTCCAGGCAAGCGGCTAGAGGCCACTGCAAGTCTGTGACAC	6878
Db	6408	ATGTCAATGAGGGCTTCAACCTTGAATCCAGCCACAGCAACAGCCGCTGTCTCAAGAGA	6467
Qy	6879	AGGCCATATGAGAACCGCAATGTCCACACACAGTGTGCCCTGTGACTTGTGCTGATGT	6938
Db	6468	TGGGCTGTGAGTAACAAGAGGGAAGCCGCCACGTGTAAAGCCGCTGTGCCACAGAT	6527
Qy	6939	CAGTACATCAGCGTGAAGCATGCGCGATGAGAGGCTTATCTTTGAGACACAGTACAGTT	6998
Db	6528	TGAAGTCAAGCTCTCAGAAACATGTCACTGAGAGGCTGTTCAGGATCCTTGAATGAATA	6587
Qy	6999	CCAGGCCCAAGCTGATGCTCATCTGTGACCTTGGCTATCTATCTGGCCAAAGGGTCAAT	7058

Db	6588	CGGTGCTCAAGATTTGCTGTAGAGCTGCAGAGTCTGTGGTAACTACTAGAAAGGCTGGAGGCTCCT	6644
Qy	7059	CCGCTGTCAAGCCCAATGGCAATATGAGAGCTTGGGGAATCTAGGCCCACTGCGCAATAT	7118
Db	6648	GCGGTGCTCAAGCCCAATGGGACGTGGAAACATAGAGATGAGAGGCCCAAGCTGTGAGATTAT	6707
Qy	7119	CTCTGTGAGAGAGTCCCGATTTCCCGCCATGGCCACCGCATCGGAACAATGTCTGTCTTA	7178
Db	6708	CTGTGTGGAAGGCTTTCTTTTCCCGCAATGGCAACAAGATTGGAAAGTTGAAAGTTGACAGTTTA	6767
Qy	7179	CGGGGCAACAGCAATCTTCTCTGCAATTCCGANTACACATGTGTGGGCTCCAGGGTGGG	7238
Db	6768	TGGGGCCACAGCTAATATTTACGTGCAAAACCGGCTACAGCTTGGGGGTCTCATGTCTAG	6827
Qy	7239	TGAATGCATATGGCAATGGGCTCTGAGTGGCTCTGAAGTCCGCTGCTTGTGACACTG	7298
Db	6828	AGAGTGTGGCAATATGGCTCTGGAGCGGACGGAACATCGAATGTCTGGCTGGCCACTG	6887
Qy	7299	TGGAGACTCTGAGCCCATTTGTCAACGGACACATCAATGGGGAGAACTACAGCTACCGGGG	7358
Db	6888	CGGTTCCCGAGACCCGATTTGTGAACGGTCTCATTTAGTGGAGATGAGGCTTCAAGTTTACAGAA	6947
Qy	7359	CAGTGTGTGTACCAATGCAATGCTGGCTTCGGCTGATCGGATGTCTGTGGCACTCTG	7418
Db	6948	CACGGTGTTTACCAAGTCAATCTGTGTTTCGGGCTTGTGGAACTTCCGTAGAGATATG	7007
Qy	7419	CCAGAGAGATCATCTGTGTGGGCAAGACCCCTTCTGTGTGCCAATTACTGTGGACA	7478
Db	7008	CTGTGAAGACCAAGATGTCTGGACAAAGCGCTGTGTGTGCCATCATCATGTGTGTA	7067
Qy	7479	CCGAGGCAACCTGTCAACGGGCTCATCTCAGGGTAAACAGTTTAACTCAACGATGTGT	7538
Db	7068	CCCTGGAAACCTCTCCCAACGGATTCATTAAATGGCAGTGAATTCACCTGAATATATGTCTGT	7127
Qy	7539	CAAGTTTGTGTGAACCCCTGGGTATATGCTGAGAGGGGCTGTAGTCCCATATGCTCTGC	7598
Db	7128	GAAATTTCATCTGCAAAACGGGCTAATTTGTGTGAGGGGGGTGTCTCGAGCCCAAGTGTGGAG	7187
Qy	7599	CAGCGGGCAATGAGATGACATGCTGCCCACTCGAGAAATCATCAACTGTACAGATCCTGG	7658
Db	7188	CAACGGCCAGTGAAGTACCCCTCTGCCACAGTGTGAGTGTGAATCTGTTCTGATCCAGG	7247
Qy	7659	AACCAAGAAATATAGTGTTCGTCAAGTTCACAGCCAGCGGGCCCGCACAGTTTACGTTCCG	7718
Db	7248	CTTTGTGGAATATGCAATTCGTTCACGGGCAACAGAACTTCCGTAGAGTTTGTAGATATGG	7307
Qy	7719	CACCACTGTCTTACCGGTGCAACACAGGCTTTACTCTCTGGGCAACCCCAAGTCTCAG	7778
Db	7308	AATGATGATCTCTGTACCAATTCAGAAAGGAAATTTTACTGTGTGGATTTCAAGCTTTGAC	7367
Qy	7779	CTGCCAGGGAATGGCAATGAGGACCGTCCCGGCCCAAGTGTCTCTTGTGTCTCTGG	7838
Db	7368	CTGTATGGCAATGGCTTATATGGACCGATCCCTGCCAAGTGTGTGGCTATATGTGTGG	7427
Qy	7839	CCATCCGGCTCCCGGCTCACTCTCCAGATGTCTGGAGACAGTTTACTGTGGAGAGCACT	7898
Db	7428	ACACCCAGGGGTCCTCTGCCAAAGCGGTCTCATCTGAGAGGTCTGTTTACTTATATGGCGCGT	7487
Qy	7899	GGTGGCGTACACTGTCAATCGGACAGCGTAACTTGTGGTGGAAACAGACCCGCAATGTGG	7958
Db	7488	CGTGCACTACTCTCTGAGAGGAGGAGGAGAGGCTCATATAGGCAACAGACAGAGTGTGCA	7547
Qy	7959	GCTGATGACACTGGAATGGCTCCCTCCTCATCTGTCAAGAAACAGCGTGGAGATTGG	8018
Db	7548	GGAAGACATCTCACTGGAGGGGGCACTGCCCATGCAACAGAAATATATCTGTGATTTCTG	7607
Qy	8019	CGGTGACCTCTGGGATTCGGGCTCATATGCAATCCGTTTGGGGGGAACAGTTTGAATCCAGGAC	8078
Db	7608	TGTGTATCCGGGGAACCCACAGCAATGGGATCTTGGCTTGTGTATGACTTTAAGACAAAGAG	7667
Qy	8079	TGTGATGAGCTTCAGTGTGAAAGCTGGGACAGTGTCTCCGGGATTCGTCAAGCGCACTGT	8138
Db	7668	TCTTCTCCGCTTCTCTGTGAAATGGGGGACACAGTGTGAGGGGCTCCCTGAACGCACTGT	7727

QY 8139 TCAAGCAATGGCTCGTGAGAGCGGCTCGAGCCGTGATGAGTATCTTTGGGAA 8198  
 Db 7728 TTTGCTCATGGTCTATGTCAGAGACTGACCCGGTGTGAGCCGTGTCTGTGGCAA 7787  
 QY 8199 CCCGAGGACTCAAGTAATGCCGAGTGTGTTCAGTATGAGCGGTGTTTCTCAGCTC 8258  
 Db 7788 CCTGGCAGCCACCAAGGAAATGATGTTCAGTATGATGGATCTGTCTCCAGCTC 7847  
 QY 8259 TATGCTATGATGCGGGGAAAGATCTAGCCCAAGGCTGTCTCAGCCGTCACTGCTC 8318  
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 QY 9158 CTCTCTGAG 9217  
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 Db 8850 AGTGAAG 8909  
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 Db 9030 AGTGAAGTGTGAG 9089  
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 Db 9264 AGATCAAG 9323  
 QY 9758 CCGTGAAG 9817  
 Db 9324 TGTGATCTTCTTGTCTTATTTATCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9383  
 QY 9818 GAG 9877  
 Db 9384 AAG 9443  
 QY 9878 CACATTTGAG 9937  
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 QY 9938 GCGGAG 9984  
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 Job time : 3122 secs

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QY 4232 CCAAGGACTATGTGTGTGGCGAGTTGCTTTTCAACGCGCTTCAACGACGTGC 4291  
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QY 5792 TGCCATTTGACATGAGGCTCGGCTCAACTCAAGCTGTGCAAGACAGAGCCCTCTGAG 5851  
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QY 5912 GAGCATGAGCCAGAAACAGTGCAGATTCAATCAACAGGCTCTCAAGTTCCACC 5971  
Db 2162 GCAACAGGCTCTGAAAGCGGCTATATGCTTCAACCAAGCTGTCTCAAGTTCCACA 2221



OY	5972	GTGATGACGACACAGGGGGGAAATCTTGGCCATAGACTTTCTCGGCTTATCACTCAACAAAT	6031
Db	2222	GCGACTTTTCAAAATGGAAGGCTTCTTGTGCTCTCAATTTTCAGAGCAATTTAGCTCAAGAAAT	2281
OY	6032	GCCCTCCTCCCAACCATCTCCCTCCCAAGCGCGAAGTGGTCACAGAGATGAAGAAATTCATA	6091
Db	2282	GTCAACCTTCCCCACGCGGTTCCACAGCGAAGAAATGCTTACAGAGATGATGATTTCCAGA	2341
OY	6092	TAGGTGACATGTCACGCTACAGATGCTTCCTGCTTACCTTAGTGGGGAATGAATTC	6151
Db	2342	TAGGAGATTTTGTGAAGTACAGATGCTCCACCCGGGTACACTTGGTGGGACCACTTC	2401
OY	6152	TGACCTGAAACTTGGAACTTACCTGCAAGTTTGAAGAGCAACCCCGATATGTAAAGTC	6211
Db	2402	TGACTTGAAGTCAAGTTCCTCCAGTTGCAAGTTTGAAGGTTCTCTCCCAACATGTGAAGAC	2461
OY	6212	ACTGTCCAACAAATAGCTTCTGACAGACTCCAAGCGGTATCTCTGAGCCAGAGTACC	6271
Db	2462	AATGCCACGCAATATGAAGTCCGAGCTGGATCATCGGAGTCAATTCTCAGTCCAGGATTC	2521
OY	6272	CTGGAAGTATCCCAAGTTCCAGACTTCTCTTGGCTGTGAAGATGAGCCCGACATA	6331
Db	2522	CGGGATATTTATTTAACTCCAGACTTCTCTTGGAGATTAAGATGGAACCAATCACA	2581
OY	6332	ACATCTCCCTCAAGTGGAGTACTTCTCAGCGAGAAACAAATATATGATTTGATTT	6391
Db	2582	ACATTACATCTTGTGTGACACATTTCAAAGTGAAGAAACATTTGATGCTACTGGAAGGT	2641
OY	6392	TTGATGTGTCATCAGAGCAGAGTCTCTGCTGAAAGCCCTGAGTGGGAATTAACAAGCT	6451
Db	2642	TTGATGTGTTCTTCTGGCAAGTCTCTGCTGATGTTAGTGGGAATCACTACTGAC	2701
OY	6452	CCCTGATGTCAACGACTCAAGCAACTGTGTATCTTGCGTTGGTCACTGATCAAGCT	6511
Db	2702	AATCAATTTTAAACAGAGAGATATCAGTTATATCTCGCTGGTCCACTACATGACA	2761
OY	6512	ACATTCGGAAGGGCTTCAAGATCCGCTATTCAGCCCCCTTACTGCAAGCTGCCAGGGCTC	6571
Db	2762	CCAGTAAAGAAAGATTCAAGATTCGCTATGACGACCTTACTGCAAGTTGACCAACCCC	2821
OY	6572	CACCTCATGGCTTCACTCTAAGGCCAGACACGACCCGCGGGGCTCCATCCACTTGG	6631
Db	2822	TGAGAAATGGGGGTATTTCTAAACAGAGCTGACAGAGCGGTGGAAGCAAGTCAATTT	2881
OY	6632	GCTGCAAGCGCGCTTACCGCCTGTGTGGGACACAGCATGGCCATCTGTACCCGCAACCCC	6691
Db	2882	TTTGCAACCTGGAATCCGAATGTGTGGCCACACAGAAATGCAACCTGTAGAGAAACCAAC	2941
OY	6692	AAGGCTACCACTGTGAGCGAAGCCATCCCTCTGTCAAGCTTTTCTGTGGGCTTC	6751
Db	2942	TTGGCATGTACCAAGTGGGACTCCCTCACGCACTGTGCAGGCTGTGTCTGTGGAAATCC	3001
OY	6752	CTGAGCCCCCAAGAAATGGAATGTGTGTTGGCAAGAAATTAACAAGTGGGAACAAAGCCG	6811
Db	3002	CAGATATCCCAAGAAACGTTTCATTTTACCGGGAGAAATTAACCTTTGACAGTAAAGTG	3061
OY	6812	TGTACAGCTGCAAGTGAAGCTTACCACTCCAGGCGAGCGCTGAGGCGCACTCAAGATGTC	6871
Db	3062	TCTAAGATGTCAATAGGGGCTTCAAGCTTGAATTCAGCCAGCAAGCAACAGCGTGTCT	3121
OY	6872	TGACACAGGCGCTATGAGCAACCGCAATGTGCCACCAAGTGTGCCCTGTGAATTGTC	6931
Db	3122	AAGAAGATGGGCTGTGAGTAAACAAGGGGAAGCCGCCCATGTGTAAAGCGGATCGCTGCC	3181
OY	6932	CTGATGTCAATGACATCAAGCGTGGAGATGGCCCATGAGGCTTATCTTTAGACACAGT	6991
Db	3182	CCAGATTTGAAGCTCAGCTCTCAGAAACATGTATCTGAGAGGCTGTGTTCAAGATCTTTGA	3241
OY	6992	ATCAGTTTCAAGGCGCAGCTGATGCTCATCTGTGACCTGTGGCTCACTACTATCTGGCCAAA	7051
Db	3242	ATGATGACGGTCTCAAGATTTGCTGAGAGCTGCAAGTCTGTGTTACTTAAGAGGCTGGA	3301
OY	7052	GGGTATCCGCTGTCAAGGCAATGGCAATGAGAGCTCGGGGACTTAAGCCCACTTGC	7111

Db	3302	GGCTTCCTCGGATGCCAGGCCCAATGGGACGTGGACATATGAGAGATGAGAGGCCAAGCTGTC	3361
Qy	7112	GAATCATCTCTGTGGAGAGCTCCCGATTCCCCCAATTGGCACCGCATGGAACTCTGT	7171
Db	3362	GA-----	3363
Qy	7172	CTGTCTACGGGGCAACAGCCATCTTCTTCCTGGCAATTCGGATATACACACTGGTGGGCTTCCA	7231
Db	3364	-----	3363
Qy	7232	GGGTGCGGTGATGCATGGCCAAATGGGCTCTGGATGGGCTTGAACTCCGCTGCTTGGCTG	7291
Db	3364	-----GCTG	3367
Qy	7292	GACACTGTGGGACTCTGAGGCCATTGTCAACGACATCATATGGGAGAACTACAGCT	7351
Db	3368	GCCACTGGGGTTCCTCCAGACCCGATTTGGAAACGGTCAATATGAGAGATGGCTTCAAGTT	3427
Qy	7332	ACCGGGGACGTGTGTGTACCAATGCAATGCTGGCTTCCGCTCATGGCATGTCTGTGC	7411
Db	3428	ACAGAGAACCGTGGTTTACCAAGTGCATCTGTGTTCCGGCTTGTGGAACTTCCGGA	3487
Qy	7412	GCATCTGCACAGAGATCATCACTGTCGGGCAAGACCCCTTCTGTGTGCATTTAATCT	7471
Db	3488	GGATATGCTCTCAAGACCAACAGTGTCTGGACAAAGCCCTGTCTGTGTCCCATACAT	3547
Qy	7472	GTGGACACCCAGGCAACCTCTGTCAACGGCCCTCACTCAGGGGTAAACAGTTTAACTCAACG	7531
Db	3548	GTGTGCACCTCGGAAACCTCTCCACGGATTTCACTAATAGGACAGTGTCAACCTGAATG	3607
Qy	7532	ATGTGTCAAGTTTGTTTGCAACCCCTGGGATATATGCTGAGGGGGCTGTAGTCCCAAT	7591
Db	3608	ATGTCTGTAAATTTCACTCGCAACACAGGGCTATTTGTGTGCAGGGGCTGTCTGCAGCCAGT	3667
Qy	7592	GCTTGGCCAGGGGGCAATGAGTGACATAGCTGCCACCTGAGATATCAACTGTATCAG	7651
Db	3668	GTCCGAGCAAGGCCAGTGGAGTACCTCTGCCCCAGTGTGAGTGTGAATCTGTGTG	3727
Qy	7652	ATCTGCACACCAAGAAATATGATGTTGGTCAAGTTCACGCGACGGGCCCGACAGTTTCA	7711
Db	3728	ATCCAGGCTTTGTGTGAAAAATGCCATTGTCTACGGGCAACAGAACTTCCCTGAGAGTTTGG	3787
Qy	7712	GCTTCCGACCACTGTGTCTTACCGGTGCAACACGGCTTCTAATCTCTCCGAGCCAC	7771
Db	3788	AGTATGGAATGATATCTGTATACATTGCAAGAGGATTTTATCTGTGGGATCTTCAG	3847
Qy	7772	TGCTCAGCTGCCAGGAGATGGCACATGGGACCGTCCCCGCCCAAGTGTCTCTTGGGT	7831
Db	3848	CCTTGAACCTGTATGGAACAAATGGCTTATGGGACCATCCCTCCCAAGTGTGTGCTATAT	3907
Qy	7832	CTGTGGCCATCCGGGGCTCCCCGCTCACTCCAGATGTCTGGAGACAGTTATCTGTGG	7891
Db	3908	CTGTGACACCCAGGGGTCCCTGTCCCAACGCGCTTCATCTGGAGAGCTGTTTACTATG	3967
Qy	7892	GAGCAGTGTGCGGTACAGTTCATTCGGCAACGCTACTCTGTGGGAAACGACCCGCA	7951
Db	3968	GCGCGGTGTGCTACATCTCTGAGAGGAGCGAGAGCTCATAGGCAACGACGAGAG	4027
Qy	7952	TGTGTGGCTGGATGGACATGGACTGGCTTCCCTCCTCACTGCTCAGGAAACGACGCTGG	8011
Db	4028	TGTGTCAAGAAAGACATCACTGAGACGGGGCACTGCCCACTGCAACAGGAATATCTGT	4087
Qy	8012	GAGTTTGGGGGACCCCTGGGATCCCGGCTCATGGCATCCGTTTGGGGGACAGCTTTGATC	8071
Db	4088	GATTCCTGGTGGATCCGGGGACCCCAACATGGGCTCTCGGCTTGTGTATGACTTTTAA	4147
Qy	8072	CAGGCACGTATGTGCTTCACTGTGTGAGCTGGCCACGTGCTCCGGGATCTGCAGAGC	8131
Db	4148	CAAGAGCTTCTCTCGCTTCTCTGTAAATAGGGGACACAGCTGAGGGGGCTCCCTGTAAC	4207
Qy	8132	GCACCTGTCAAGCCATATGGCTGTGTGAGACGGGCTGCAGCTGTAATGTGAACTTCTT	8191

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 Db 4988 NNN 5047  
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 Db 5048 NNN 5107  
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RESULT 2  
 AY407075  
 LOCUS  
 DEFINITION  
 Mus musculus CSMD1 gene, VIRUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 5901)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.B., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.C.,  
 Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL  
 Science 302 (5652), 1960-1963 (2003)  
 PUBMED  
 14671302  
 2 (bases 1 to 5901)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
Fertig, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D., and Cargill, M.

TITLE  
JOURNAL  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
Location/Qualifiers

source

1..5901

/organism="Mus musculus"

/mol\_type="genomic DNA"

gene

/db\_xref="taxon:10090"

<1..>5901

/gene="CSMD1"

/locus\_tag="Hm2769"

ORIGIN

Query Match 19.8%; Score 2011.6; DB 9; Length 5901;

Best Local Similarity 58.0%; Pred. No. 0;

Matches 3609; Conservative 0; Mismatches 2290; Indels 328; Gaps 7;

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2 TGGAGCCGAGTTATGATCTTCTCCATATCTAGAGGGGAGAGCTCCACAGCCCACTGA 61  
3812 TAGAAGCTTCTATGCTGCCACTCCAGCCGCGATTTGAAGACAGACAGAAAGCTCT 3871  
62 TTGGAAGTTTCCAGGGCTCTCAAGCCCGAGAGAGATCGAGACAGTGTAAACGCTCT 121  
3872 TCCTGCGCTTCCGAGCGATGATCTGTGAGCAATGCTGCTTCTGATTAATATACAG 3931  
122 TTCTGCGCTTCCGAGCGATGATCTGTGAGCAATGCTGCTTCTGATTAATATACAG 3931  
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3992 CGAAGCTGAAGCTGGGCTCTCCGCTCACTCACTCACTCACTCACTCACTCACTCACT 4051  
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302 ATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 350  
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351 -----GCACTCTGTGAGGCGCAATACAGGCTCGAGGGGATGTTTGT 396  
4172 CCCCCAATGCCCCAGAACTACACAGTGAAGATCTGCTTGTATTTTGTATCTGTG 4231  
397 CACCAAACTACCTCTCACTACACAGCTGGGAGATGTCATCTATTCATCAACGCTG 456  
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457 CCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 516  
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517 CAGAGTTGTTGATGGAACATCCCAAGCCAGGCT----- 553  
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969 CCGGATCCAGATCCAAAGTTGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1028  
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1509 ATTCTCACTGAAGCAACCAAGTATGAAATCCGGAATGAGCCCTTATGAGCA 1568  
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Qy	5972	GTGATGCAAGCCACAGGGGGAACTTTGSCCATAGCTTTCTCCGCTTATCTCACTCACAAT	6031
Db	2169	GGGATTTCTCCAAATGAGGCTTCTTTGTCTCTCAATTTTCATGATTCATTCAGTGAAGGT	2228
Qy	6032	GGCCTCTCTCCCAACATCCCTCCCCCAACGCGGAAAGTGTACAGAAATGAAATTCATA	6091
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Qy	6092	TAGGTGACATGTGTAGCTTACAGATGCTCCCTGGCTTTACCTTATGTGGGGAATGAAATTC	6151
Db	2289	TAGGGGAACTTGTGAAGTACAGGTGCTCATCCAGGGTACATTTGTGGAAAGCAACCC	2348
Qy	6152	TGACCTGAAACTTGGAACTTACCTGTGCAAGTTTGAAGAACACCCCCCAATTTGTGAAGTC	6211
Db	2349	TGACATGCAAGTCACTCAAGCTCAAGCTACGTTTCAAGGCTTCCACCACTGTGAAAGCAC	2408
Qy	6212	ACTGTCAACAAATAGCTTCTGACAGACTCACAAGCGGTATCTCAGCCAGAGCTAC	6271
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Qy	6272	CTGGAAGTATCCCAAGTTCAGACCTGCTCTTGGCTGTGAGAGTGAAGCCCGACTATA	6331
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Qy	6332	ACATCTCCCTCAAGTGAAGTACTTCTCAGACGAAAGCAATATGATGAATTTGAATTT	6391
Db	2529	ACATCAACCTTTTGTGTGACACATTTCCAAAGTGAAGAAACAAATTTGATGACTGAAGTGT	2588
Qy	6392	TTGATGTGTCAATCAGAGACAGTCTCTGTGTAAGGCCCTCAGTGGAAATTACTCAAGTC	6451
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Qy	6512	ACAATCGAAGGGCTTCAAGATCCGCTATTCAAGCCCTTACTCAGACTGCCCCAGAGGCTC	6571
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Qy	6572	CACCTCAATGGCTTATCCTTAGGCCACAGACCAACCCCGGGGGCTTCATCTCACTTGG	6631
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Qy	6872	TGGACACAGGCGCTATGGAGCAACCGCAATGTCCACACAGTGTGTCCCTGTGACTTGTG	6933
Db	3069	AAGAAATGAGCCCTGTGGAGCAACAAGGAAAGCCACCAATGCAAAACCGGCGCCCTGCC	3128
Qy	6932	CTGATGTCAGTAGCATTCAGCCGTGAGACATGCGCCGATGGAGGCTTATCTTTGAGACAGT	6991
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Qy	7052	GGGTATCCGCTGTGAGGCCAATGGCAATGGAGCTCGGGGACCTTACCGGCCACTGCGC	7111
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Qy	7232	GGGTGCTGATGTCATGGCAATGGGCTCTGAGTGTCTCTGAATGCTCGCTGCTTGTG	7291
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 Qy 8192 GTGGGAACCTTGGGATCTCCAAATATGCTCCGAGTTGTGTTCAATGATGCTGTGTTCT 8251  
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 Qy 8252 CCAGCTCTATCTGTATGATGTCGCGGAGAGATACACGCGACAGGCTGCTGACCGCT 8311  
 Db 4275 CCAGCTCTGTATCTATGCTGTGCTGAGGAGGCTACAAAGCTGCGGGCTATGATCTGCG 4334  
 Qy 8312 ACTGCTGTGATCAATGATGCTGAGCAGGCACTGAGTGCCTGTGATTAATCTG 8371  
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 Qy 8732 CTGTGTCTCCGCTCCCGTGGAGAGAGAGACCGAGGCTTCTCTACAGGTCAATGTCT 8791  
 Db 4735 -----GCGGTCT 4741  
 Qy 8792 CTTTCTGTGCAATCCCTCTGTGCTGTGAGGCTCTCCACGAGGTTTTCAGAGCAG 8851  
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 Db 4862 NNN 4921  
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 Db 4922 NNN 4981  
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 Qy 9811 AGCAGAGGAGAAACCAAGTCTTCAATGAGGATATGAGGCGAGAGAACCAAGT 9870  
 Db 5735 AACACAGAAACCAAGAGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5794  
 Qy 9871 TTGCGGCACTTTGAGAAACCAATGTACAGACCGCAACATCCAGCCACAGACATATG 9930  
 Db 5795 GACAGCTTCAATTTGAAGCCCATGTATATCAAACTTAAGAACCAAGAGGAGGCAAG 5854  
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 Db 5855 CTGTGAGTTTGAACAGACTCTGAACACAGTGTGTACAGGTATAG 5901

RESULT 3  
AK081081  
LOCUS  
DEFINITION  
AK081081 3882 bp mRNA linear HTC 03-APR-2004  
Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length  
domains 1, full insert sequence.  
AK081081  
ACCESSION  
AK081081.1 GI:26099665  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS  
TITLE  
Carninci, P. and Hayashizaki, Y.  
JOURNAL  
MEDLINE  
PUBMED  
99279253  
10349636  
2  
REFERENCE  
AUTHORS  
TITLE  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
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prepare full-length cDNA libraries for rapid discovery of new genes  
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P.,  
Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
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Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, M.,  
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RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL  
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AUTHORS  
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The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
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The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL  
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Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P.,  
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Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shitaki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
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Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
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 1 (bases 1 to 5824)  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,  
 Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
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 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
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[illegible]

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DEFINITION	DKRZP668H06203_r1 686 (synonym: h1ccs) Homo sapiens				
DEFINITION	DKRZP668H06203_5', mRNA sequence.				
ACCESSION	BX478219				

VERSION	BM478219.1	GI:31912870
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 651)	
AUTHORS	Ansoezge,W., Krieger,S., Regiert,T., Rittmuellet,C., Schwager,B., Mewes,H.W., Well,B., Amlid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.	
TITLE	EST (Ansoezge,W., Krieger,S., Regiert,T., Rittmuellet,C., et al.)	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: MIPS	

**FEATURES**

Ingolsaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert.  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by EMBL (European Molecular Biology Laboratories,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp66H06203) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcententrum, Neuherweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

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/lab_host="DH10B"
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cDNA-collection"

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## ORIGIN

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			100.0%;	Pred. No. 1.5e-144;				
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							Gaps	0;
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QY	9313	TGATTCCTGGGGAGATGTTTTGGCCAAAGAAATCCCTGTGTGGAAAGGGGGCCTATGAATPACAGG						9372
DB	77	TGATTCCTGGGGAGATGTTTTGGCCAAAGAAATCCCTGTGTGGAAAGGGGGCCTATGAATPACAGG						136
QY	9373	GGAAGAACACAGCCACGCCATGCTCAGAGTGACTGGCTTCCAAGTTGCCACAGCAGAGGTCA						9432
DB	137	GGAAGAACACAGCCACGCCATGCTCAGAGTGACTGGCTTCCAAGTTGCCACAGCAGAGGTCA						196
QY	9433	ATGCCACCAATGATGCAACACAGTGGCGGTGGAGCTGCACTTGGCTGGAACTTAACAAGAAG						9492
DB	197	ATGCCACCAATGATGCAACACAGTGGCGGTGGAGCTGCACTTGGCTGGAACTTAACAAGAAG						256
QY	9493	AAGATTTTCATCTCTCTACTCCAGGTGTACACAGATTACAGGGCGTGTGAGATCTTTATGA						9552
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DB	437	GACTGGAACCTCAGGCTGCTGGAGTCAGACCCCGAGTCATTTTGCCGCACTTTTGCTTCCA						496

QY 9733 ACAGAGCTCAGTGGAGCGGAGTCCGTGCTTTCATCGCCCTCATTTATTTGGGGCT 9792  
 DB 497 ACAGAGCTCAGTGGAGCGGAGTCCGTGCTTTCATCGCCCTCATTTATTTGGGGCT 556  
 QY 9793 TCGTCTCATCTCTACAGCAGAGAGAGAGCCAAAGTTCCTTTCATGCTATGCTG 9852  
 DB 557 TCGTCTCATCTCTACAGCAGAGAGAGAGCCAAAGTTCCTTTCATGCTATGCTG 616  
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LOCUS CF744273 748 bp mRNA linear EST 10-OCT-2003  
 DEFINITION UI-M-GVO-clis-b-24-0-UI.r1 NIH\_BMAP\_gvo Mus musculus cDNA clone  
 IMAGE:30620879 5', mRNA sequence.

ACCESSION CF744273  
 VERSION CF744273.1 GI:37640612  
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Dr. James Lin, University of Iowa  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/mouseefi.html  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5,  
 Location/Qualifiers

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 /note="Organ: Brain; Vector: pYX-Asc, Site\_1: Bcor I; Site\_2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGACTGAT. This library was created for the University Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

## ORIGIN

Query Match 6.1%; Score 622; DB 7; Length 748;  
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 Matches 675; Conservative 0; Mismatches 73; Indels 1; Gaps 1;

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 QY 6895 CGCAATGTCCACACACAGTGTGCTCTGTGACTTGTCTGATGTGATGATCAGTACGCTG 6954  
 DB 61 AGCAATGTCCCCCTCAGTGTGCTCTGTGACTTGTCTGATGTGATGATCAGTACGCTG 120  
 QY 6955 GAGCATGGCCGATGAGAGCTTATCTTTGAGACACAGTATGATGATGATGATGATGATGATG 7014  
 DB 121 GAGCAGGCGCGGTGAGAGCTATCTTTGAGCCAGATGATGATGATGATGATGATGATGATG 180  
 QY 7015 CTCAATCTGTGACCTGTGCTACTATGATGATGATGATGATGATGATGATGATGATGATG 7074  
 DB 181 CTCAATCTGTGACCTGTGCTACTATGATGATGATGATGATGATGATGATGATGATGATG 240  
 QY 7075 GGCATATGAGAGCTGTGAGAGCTTACAGCCCACTGTGCGCATATCTCTGTGAGAGCTC 7134  
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 QY 7135 CGAATTCCTCCCATGAGCGCAAGGATGAGAGACAGTGTGCTACGAGGCAAGAGCATC 7194  
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 QY 7255 GGGCTCTGAGTGTGCTGAGAGTCCGCTGCTTGTGATGATGATGATGATGATGATGATG 7314  
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 QY 7315 ATTGTCAGAGACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7374  
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 QY 7375 TGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7434  
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 QY 7435 TGTGCGGCAAGACCCCTTTCTGTGTGCAATTAACCTTGTGATGATGATGATGATGATG 7494  
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 accession0361.d.22 5prim, mRNA sequence.

ACCESSION BX671124 GI:37982337  
 VERSION BX671124.1  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 673)  
 Soares,M., Bonaldo,F. and Hately,F.  
 A Pig Normalised Multi-Tissue cDNA Library  
 Unpublished (2003)  
 CONTACT: Tosser-Klopp G

TITLE JOURNAL  
 COMMENT Institut National de la Recherche Agronomique

Chemin de Borde-Rouge - Auzeville BP27, 31326 Caetanet-Tolosan cedex, FRANCE  
 Tel: 33 (0) 5 61 28 51 14  
 Fax: 33 (0) 5 61 28 53 08  
 Email: tosseer@toulouse.inra.fr  
 Sequence cleaned of vector, adaptor and repetitions. Contact us at [aisgenasupport@jouy.inra.fr](mailto:aisgenasupport@jouy.inra.fr) to obtain the chromatogram of this sequence.  
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## FEATURES

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Location/Qualifiers

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## ORIGIN

Query Match 5.5%; Score 558.6; DB 5; Length 673;  
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2919 AGGAAACCCCAAGTTGGTCTACAAAGTTGATGAGATGATTTTTCAGAGAGCTCCGT 2978  
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2979 GTCCTTCAGCTGTGACCTTGATATACAGCTTCGAGGATGATGAGAGAGCTGTGTGAG 3038  
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3039 TGGAGAGCCCGGACCTTGAGACCGGCTCTGCCCACTGTGTGCGGAGTGTGAGAGGAC 3098  
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3099 AGTGAAGAGAGAGTGTGCGGAGAGTGTGTCAACCGGAGATTCAGCTCCATATGAACA 3158  
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3159 CAATCTCACTGATCTGACCAATCGAAGAGAGAGGCGGCTGACCAATTTGGGCTACACTT 3218  
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 IMAGE:30356213 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 NIH-MGC <http://imgc.nci.nih.gov/>  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pyx-5.

## FEATURES

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Location/Qualifiers

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/clone\_lib="NIH BMAP FY0"

/note="Organ: Brain; Vector: pyx-Asc; Site\_1: Ecor I; Site\_2: Not I; The library was constructed according to Bontalido, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

## ORIGIN

Query Match 5.4%; Score 546; DB 7; Length 666;  
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8438 CATATCAGTGTGTCTCTGCTATATATGATGAGTCAATAGAGTATCTGTGCTGAGCTGCA 8497  
 61 CATATCAGTGTGTCTCTGCTATATATGATGAGTCAATAGAGTATCTGTGCTGAGCTGCA 120



QY	8498	CCAAAGACCCGACATGGAAATGGAACCAAGCCCGCTGGAAAGCTCATATGGCAAGCAC	8557
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QY	8738	TCCGCTCCCGTGGAGAGAGAGAACCCAGGCTTCTCTTACAGTCACTGTCTTCTTCT	8797
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QY	9038	ACCTGA 9043	
Db	661	ACCTGA 666	
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DEFINITION	quadrigenema Mus musculus cDNA clone B230309H22 3', mRNA sequence.		
ACCESSION	BB309178		
VERSION	BB309178.2	GI:16402481	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus		
AUTHORS	1 (bases 1 to 659)		
	Arakawa, T., Carinci, P., Fukuda, S., Furuno, M., Hanagaki, T.,		
	Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,		
	Komno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,		
	Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,		
	Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,		
	Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,		
	Takeda, Y., Tanaka, T., Toyai, T., Muramatsu, M. and Hayashizaki, Y.		
TITLE	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)		
JOURNAL	Unpublished (2001)		
COMMENT	On Jul 10, 2000 this sequence version replaced gi:9009883.		

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1-7-22 Suicho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel.: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@ec.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci,F., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. , 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,  
Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.  
and Hayashizaki,Y.  
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Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,  
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Computer-based methods for the mouse full-length cDNA  
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nonredundant cDNA library. Genome Res. , 11 (2), 281-289 (2001)  
Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamataka,I.,  
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and  
Hayashizaki,Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN,  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

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/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGGAGAAGATCCAGACGCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGGAATTTCGACGTAAATAATTAATTCGCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pluescript KS(+) after bulk excision from Lambda F.I."	

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ORIGIN	
Query Match	5.1%; Score 519.6; DB 2; Length 659;
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2633	ATAACAATCATGATGCATCTACTTCATCCAGACCAGCCAGGAGGAGGAATTCAGCTGA 2692
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67	ATAACAACCAACGAGTGATCTACTTCATCCAGACCAGCCAGGAGGAGGAATTCAGCTTA 126
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2693	AAGCCAGGGCATTCGAACTCTCCGAGGAGATGTCTCAAGGTTTATGATGGCACACAA 2752

Db 127 AACCAAGGATTTGAGCTGCTGAAAGAGACCTCCTCAAGCTTATGACGCACTAACA 186  
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 Db 247 GCACGCTAGCACTGTGGCTTGAATTTCACTGATGCTGAAAACACAGCAAGGCT 306  
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 Sushi domain / SCR repeat / CCP module/ CUB domain containing  
 protein, full insert sequence.  
 ACCESSION  
 AK046385  
 VERSION  
 AK046385.1 GI:26091501  
 KEYWORDS  
 HTC; CAP trapper.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 JOURNAL  
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 PUBMED  
 99279253  
 10349636  
 REFERENCE  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 JOURNAL  
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 20499374  
 11042159  
 REFERENCE  
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
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 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
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 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watanabe, M.,  
 Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer

JOURNAL  
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 20530913  
 11076861  
 REFERENCE  
 4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 JOURNAL  
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 REFERENCE  
 5 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 JOURNAL  
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 PUBMED  
 11076861  
 REFERENCE  
 6 (bases 1 to 2841)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuta, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirose, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,  
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohse, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submision  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
 COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/.  
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**ORIGIN**

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REFERENCE	1 (bases 1 to 671)		
AUTHORS	Bonnet,M., Tosser-Klopp,G., Benne,F., Cabau,C., Vallegier,S.,		
	Soares,A., Bonnaud,F. and Harey,F.		
	A pig Normalised Multi-tissue CDNA Library		
TITLE	Unpublished (2003)		
JOURNAL	Contact: Tosser-Klopp G		
COMMENT	Genetique Animale		
	Institut National de la Recherche Agronomique		
	Chemin de Borde-Rouge - Auzeville BP27, 31326 Casanet-Tolosan		
	cedex, FRANCE		
	Tel: 33 (0) 5 61 28 51.14		
	Fax: 33 (0) 5 61 28 53.08		
	Email: tosser@toulouse.inra.fr		

**FEATURES**  
**SOURCE**

```

FEATURES
source
Sequence cleaned of vector, adaptor and repetitions. Contact us
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Query Match	4.5%;	Score 453.2;	DB 5	Length 671;
Best Local Similarity	92.6%;	Pred. No. 8.6e-100;		
Matches 476;	Conservative 0;	Mismatches 38;	Indels 0;	Gaps 0;

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Qy	5477	CAGATTCAACTGGAGTATGATGAGGCTTATGAACTTCAAGAGTGGCCAGACCCAGAGCCCT			5538
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Db	361	TTGGCAATGAGATGTGAAGGGGTGTGGCTCAACAGTGGGCAAGTGTAACTTGCAGT			420
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Db	421	GCTTCCGGGGGTATCAACTGATGTGGGCCACCTGTCTTCAATATGTCAAGCACGGCACCAAC			480
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Db	481	GGAATCGGAGCAACCCCTGTGCCAAGTGTGAAGT			514
RESULT 13					
LOCUS	BU370222	733 bp	mRNA	linear	EST 28-NOV-2002
DEFINITION	603595953571 CSEQCHN73 Gallus gallus cDNA clone CHEST563e9 5', mRNA				
ACCESSION	BU370222				
VERSION	BU370222.1				
KEYWORDS	EST.				
SOURCE	Gallus gallus (chicken)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 733)  
Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,  
Fong, W. T., Tickle, C., Brown, W. R., Wilson, S. A. and Hubbard, S. J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
2235534  
MEDLINE  
PUBMED  
12445392  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers  
1. 733  
/organism="Gallus gallus"  
/mol\_type="rRNA"  
/strain="Compton line 151"  
/db\_xref="taxon:9031"  
/clone="CHES1563e9"  
/sex="Female"  
/tissue\_type="not cerebrum or cerebellum"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQC/N73"  
/note="Organ: Brain; Vector: pBluescript II KS(+); Site\_1:  
EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand reaction, double-stranded cDNA  
Following this first strand reaction, double-stranded cDNA  
was bluntended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

ORIGIN

Query Match 4.4%; Score 444.2; DB 5; Length 733;  
Best Local Similarity 78.0%; Pred. No. 1.5e-97;  
Matches 572; Conservative 0; Mismatches 158; Indels 3; Gaps 3;

QY 8365 AACTGTGTGACCTGTGGATTCAGGCAATGCGCTTGGGCAATGACTTCAGGTAC 8424  
Db 2 AACTGCGGTGACCGAGTGTGCGACGCAACGGCATTAAGCTGGGCAATTTTACCTNC 61

QY 8425 AACAAACTGTGACATATCATGTGTGCTGCTATATGATGAGTGCATAGAGTATCT 8484  
Db 62 AACAAACAGTGTGTTCAGTGCATGCTGGGTATGATGAGTGCAGACAGACATCC 121

QY 8485 GTGTGAGTGTGACCAAGGACCGGACATGAGTGAACCAACCGCTGTGCAAACTCTC 8544  
Db 122 TCTGTGATGTGTACAAAGACGAACTGTGAGTGAACCAACCGCTGTGCAAACTCTC 181

QY 8545 ATGTGCAAGCCACTTCCTCCGCTATCCCAATGAGGAAGTGTGGGGTGTGACTTCATGATG 8604  
Db 182 ATCTGTAAACCCCAACAGCCATCCCAATGAGGAAGTGTGGGGTGTGACTTCAGCTGC 241

QY 8605 GGCTCAAGTGTATCTTATGCTGCTGTGAGGGGTATCCAGCTCTCCCTGCGGGGTGTC 8664  
Db 242 GGCTCAGAGTGTATGCTGCTGCTGTGAGGGGTATCCAGCTCTCCCTGCGGGGTGTC 301

QY 8665 AACTGTGAGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 8724  
Db 302 AACTGTGAGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 361

QY 8725 GGGATCTGTGATGTCCTCCCTCCGAGAGAGAGACGAGGCTTCTCTACAGGTCA 8784  
Db 352 GGAATTCAGG-ATTCCTGCCCCAGGCGCGGGAGAGACCGAGCTTACAGTACCGCTCC 420

QY 8785 TCTGTCTCTCTCTCTCTGCGCATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8844  
Db 421 TCTGTGCTCTCTCTCTCTGCGCATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480

QY 8845 CAGTCAATGTGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 8904  
Db 481 CAGTCAATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540

QY 8905 TGTGCGACCTGTGATGTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 8964  
Db 541 TGTGAGACCTCCGCGGTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600

QY 8965 GGAGACAGTCT 9024  
Db 601 GGAAGCATGATTTTCTTCAAGTGCAGAGAGGGTAACT-CTGACAGGCTCCACCA-CAAG 658

QY 9025 AACTGCTCCCAACCTGACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 9084  
Db 659 AACTGCTCCCAACCTGACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 718

QY 9085 AGGACCCAGAGA 9097  
Db 719 AAGCAGCTGAAA 731

RESULT 14  
A1928999  
LOCUS  
DEFINITION  
aushb10.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone  
IMAGE:2519011 5' similar to SW:BNP1\_MOUSE P98063 BONE MORPHOGENETIC  
PROTEIN 1 PRECURSOR ; mRNA sequence.  
A1928999  
A1928999.1 GI:5664963  
EST.  
Homo sapiens (human)  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 458)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacey, M., Le, N., Lennon, G., Marra, M.,  
Martin, J., Moore, B., Scheinberg, K., Seftone, M., Tan, F.,  
Teisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: eest@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: -40RP from Gibco  
High quality sequence stop: 429.  
Location/Qualifiers  
1. 458  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2519011"  
/sex="male"  
/tissue\_type="frontal lobe"  
/dev\_stage="5 months post-conception"  
/lab\_host="DH10B"  
/clone\_lib="Schneider fetal brain 00004"  
/note="Organ: brain; Vector: pBluescript SK (Stratagene);  
Site\_1: SstI; Site\_2: XhoI; Double-stranded cDNA was  
prepared from human fetal brain tissue. 5' and 3'

FEATURES  
source

adaptors were used in cloning as follows: 5' adaptor sequence:

5'-GAGAGAGAGAGAGCTCAAGATCCTTAATTAATTATATCCCCCCCC-3' and 3' adaptor sequence: 5'-GAGAGAGAGAGCTCAAGATTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."

## ORIGIN

Query Match 4.3%; Score 440; DB 1; Length 458;  
Best Local Similarity 99.8%; Pred. No. 1.4e-96;  
Matches 451; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 5560 GCTGGCTACACGTTGGGACATCATGACCTTGAGTCCCTCCGGGGATCAATTGACT 5619  
DB 7 GCTGGCTACACGTTGGGACATCATGACCTTGAGTCCCTCCGGGGATCAATTGACT 66  
QY 5620 GGGCACCCTCTCTCTCACTGTCATCAATGACCAACCGAATGGACCAACCCCTGCCCC 5679  
DB 67 GGGCACCCTCTCTCTCACTGTCATCAATGACCAACCGAATGGACCAACCCCTGCCCC 126  
QY 5680 AAGTGTGAAGTCCCTTGGGGGAAACATCACTTCTTCCAAAGGCACTGTGTACTCCCGG 5739  
DB 127 AAGTGTGAAGTCCCTTGGGGGAAACATCACTTCTTCCAAAGGCACTGTGTACTCCCGG 186  
QY 5740 GGGTTCCTTAGCCCTGAC-TCCAGCTCCCAAGACTGTGTCTGCTGATCAACCGTGCCAT 5798  
DB 187 GGGTTCCTTAGCCCTGAC-TCCAGCTCCCAAGACTGTGTCTGCTGATCAACCGTGCCAT 246  
QY 5799 TGGCCATGGGCTCCGCTCACTCACTGCTGTCAGACAGAGCCCTTGGAGATTTCAT 5858  
DB 247 TGGCCATGGGCTCCGCTCACTCACTGCTGTCAGACAGAGCCCTTGGAGATTTCAT 306  
QY 5859 CACCATCTGGGATGGGCAACAGCAACAGCAACGCGCTGGGGCTTTCACCCGGAGCAT 5918  
DB 307 CACCATCTGGGATGGGCAACAGCAACAGCAACGCGCTGGGGCTTTCACCCGGAGCAT 366  
QY 5919 GGGCAAGAAAACAGTGCAGATTTCATCAACCAAGTCTGCTCAAGTTCACCGTGATGC 5978  
DB 367 GGGCAAGAAAACAGTGCAGATTTCATCAACCAAGTCTGCTCAAGTTCACCGTGATGC 426  
QY 5979 AGCCACAGGGGGATCTTCCCAATAGCTTCT 6010  
DB 427 AGCCACAGGGGGATCTTCCCAATAGCTTCT 458

RESULT 15  
CKJ12578 707 bp mRNA linear EST 01-MAR-2004

LOCUS SB02035A2B11.f1 normalized Keck-Tagu library SB02 Taeniolypgia  
DEFINITION gutata cDNA clone SB02035A2B11.f1 5, mRNA sequence.

ACCESSION CKJ12578  
VERSION CKJ12578.1 GI:44822152

KEYWORDS EST.  
SOURCE Taeniolypgia gutata  
ORGANISM Taeniolypgia gutata

REFERENCE Archosaures; Aves; Neognathae; Passeriformes; Estrildidae;  
Estrildinae; Taeniolypgia.  
1 (bases 1 to 707)

AUTHORS Claydon, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M.,  
Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.  
and Liu, L.

TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource  
for Study of Genes, Brain, and Behavior

JOURNAL Unpublished (2004)

COMMENT Contact: David F. Clayton  
University of Illinois  
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA

Tel: 217 244 3668  
Fax: 217 244 1648

Email: claydon@uiuc.edu

Base Calling/Quality Scores: PHRED from Washington University

Genome Center.

Vector Trimming: Cross match from Washington University Genome  
Center PHRAP suite. Low quality bases (Phred score < 20) were  
trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded  
by PHS grant # R01 NS045264, 'Songbird Neurogenomics Initiative'.

PCR Primers

FORWARD: TAATACACTCACTATAGGG (77)

BACKWARD: ATTACCTCACTAAG (73)

Insert length: 707 Std Error: 0.00

Plate: SB02035A2 row: B column: 11

Seq primer: TAATACACTCACTATAGG (77)

High quality sequence stop: 707.

Location/Qualifiers

1..707

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/mol\_type="mRNA"

/db\_xref="taxon:59729"

/clone="SB02035A2B11.f1"

/issue\_type="brain"

/dev\_stage="late embryo, post-hatch days 1, 10, 20, 45,  
and adult (pooled)"

/lab\_host="DH10B"

/clone\_lib="normalized Keck-Tagu Library SB02"

/note="Organ: brain; Vector: PHS II SK(+); Site 1:  
EcoRI(5' side of insert); Site 2: NotI (3' side of  
insert); The library was constructed and normalized as  
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.  
(1996), Genome Research 6(9): 791-806. An identifying tag  
was added at the 3' during cDNA synthesis:  
insertAAAAAAAAAAAAAAAAAATGCGA."

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insertAAAAAAAAAAAAAAAAAATGCGA."

insertAAAAAAAAAAAAAAAAAATGCGA."

insertAAAAAAAAAAAAAAAAAATGCGA."

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insertAAAAAAAAAAAAAAAAAATGCGA."





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 10:04:46 ; Search time 27137 Seconds  
(without alignments)  
17663.279 Million cell updates/sec

Title: US-10-016-248-1

Perfect score: 10136  
Sequence: 1 atggcgagggcgccctccccc.....tcgacggcgccgacgcgcac 10136

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database :

GenEmb1:\*  
1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10136	100.0	10136	6	AX685957 Sequence
2	8718.6	86.0	13113	6	AY210418 Homo sapi
3	7616.4	75.1	8010	6	AX685958 Sequence
4	4348	42.9	11221	10	AY017475 Mus muscu
5	4260.4	42.0	6004	6	AX537467 Sequence
6	4199.4	41.4	11580	9	AF333704 Homo sapi
7	4183.2	41.3	12525	6	AX374893 Sequence
8	4067.4	40.1	10433	6	AX374896 Sequence
9	4067.4	40.1	10673	6	AX374891 Sequence
10	3597.8	35.5	3896	6	AX149475 Sequence
11	3561.8	35.1	3905	6	AX149473 Sequence
12	3443	34.0	4380	9	AK127722 Homo sapi
13	3435.6	33.9	13040	9	AB114605 Homo sapi
14	3435.6	33.9	13148	9	AB114604 Homo sapi
15	3387.8	33.4	10944	9	AY017307 Homo sapi
16	3184.8	31.4	12486	9	AY210419 Homo sapi
17	2988.6	29.5	10774	9	AB067481 Homo sapi
18	2865.8	28.3	9120	10	AK122567 Mus muscu
19	2715.4	26.8	7323	6	AX306890 Sequence

20	2715.4	26.8	8034	6	AX306891 Sequence
21	2671	26.4	6409	6	AX306888 Sequence
22	2503.6	24.7	5598	6	AX306886 Sequence
23	2479	24.5	5463	9	AB067471 Homo sapi
24	2450.8	24.2	5667	6	AX306889 Sequence
25	2450.2	24.2	6145	6	AX306887 Sequence
26	1773.2	17.5	3715	9	AY358174 Homo sapi
27	1658.2	16.4	3312	6	CO842383 Sequence
28	1658.2	16.4	3312	6	AK122603 Homo sapi
29	1569	15.5	3810	6	AX833690 Sequence
30	1569	15.5	3810	9	AK095627 Homo sapi
31	1538.4	15.2	3289	9	AB067477 Homo sapi
32	1475.6	14.6	1866	6	CO726903 Sequence
33	1371.6	13.5	2387	6	AX743686 Sequence
34	1316	13.0	3915	6	CO734404 Sequence
35	1170	11.5	3989	9	AK126936 Homo sapi
36	1147.4	11.3	3518	9	AK127129 Homo sapi
37	1128	11.1	3490	9	AK126857 Homo sapi
38	1031.2	10.2	1615	6	AX492983 Sequence
39	982.6	9.7	2334	6	CO726904 Sequence
40	783.6	7.7	2609	6	AX477377 Sequence
41	733.8	7.2	1135	6	AX179316 Sequence
42	557.6	5.5	3726	6	AX833409 Sequence
43	557.6	5.5	3726	9	AK095111 Homo sapi
44	384.6	3.8	1830	6	CO843307 Sequence
45	384.6	3.8	1830	9	AK126252 Homo sapi

#### ALIGNMENTS

RESULT 1	AX685957	10136 bp	DNA	linear	PAT 29-MAR-2003
LOCUS	AX685957	Sequence 1 from Patent WO02064791.			
DEFINITION	AX685957				
ACCESSION	AX685957				
VERSION	AX685957.1	GI:29371852			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	1 Alsobrook II, J.P., Anderson, D.W., Burgess, C.E., Boldog, F.L., Casman, S.J., Coleman, S.D., Edinger, S.R., Ellerman, K., Gerlach, V., Gorman, L., Grose, W.M., Guo, X., Herrmann, J.L., Kexda, R., Lepley, D.M., Li, L., Macdougall, J.R., Miller, I., Pena, C.E., Peyman, J.A., Rastelli, L., Rieger, D.K., Shimkets, R.A., Smithson, G., Szytek, K.A., Stone, D.J., Tchernev, V.T., Vernet, C.A., Voss, E.Z., Zelnutzen, B.D., Zhong, H. and Zhong, M.				
TITLE	Proteins and nucleic acids encoding same				
JOURNAL	Patent: WO 02064791-A1 22-AUG-2002;				
Curation	Curation Corporation (US)				
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source	1. 10136				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Query Match	100.0%;	Score 10136;	DB 6;	Length 10136;	
Best local similarity	100.0%;	Pred. No. 0;			
Matches 10136;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGGCGGGCGCCCTCCCGCTTGGCTGCTGCTGAGTTGATCTCAAGCTGCTGT	60		
DB	1	ATGGCGGGCGCCCTCCCGCTTGGCTGCTGCTGAGTTGATCTCAAGCTGCTGT	60		
QY	61	GCTAGCAATCAGGAGACATCTCGTGGCGCTAGACCTCCGAGCTAGTCAAGCAAAAT	120		
DB	61	GCTAGCAATCAGGAGACATCTCGTGGCGCTAGACCTCCGAGCTAGTCAAGCAAAAT	120		
QY	121	GAGTTAAGTCTCAGGTGTGAAGCTGATGCCAGCAAGACAGCCAGAACGCTCT	180		

Db	121	GAGTTGAAGTCTCGAGGTGTGAAGCTGATGCCAGCAAGCAAGCAACAGCCAGAACAGCTCT	180
Qy	181	GTGTTAACTCAGGTTGTGTGTGTCCCAAGACATATATGTGTCCAGACCCCTGGCATACC	240
Db	181	GTGTTAACTCAGGTTGTGTGTGTGCCCAAGACATATATGTGTCCAGACCCCTGGCATACC	240
Qy	241	GAAGGGGCAAAAGCTAGGCTCCGATTTTCAGGTTAAGATCCACGTCAGATTCACTGCG	300
Db	241	GAAGGGGCAAAAGCTAGGCTCCGATTTTCAGGTTAAGATCCACGTCAGATTCACTGCG	300
Qy	301	AACGAGGGCTATGACCTCGCAAGGGTCCAAAGCGGATCACTGTATGAAGTAGGCGCATG	360
Db	301	AACGAGGGCTATGACCTCGCAAGGGTCCAAAGGGATCACTGTATGAAGTAGGCGCATG	360
Qy	361	TTTGGCGCTTGAGAGCGACCAAGGCTGACCGAGTCTGCCGAGTGTGTGATGCCACCTT	420
Db	361	TTTGGCGCTTGAGAGCGACCAAGGCTGACCGAGTCTGCCGAGTGTGTGATGCCACCTT	420
Qy	421	CGAGGCCCCCTGGGGCATCATCACTCCGCCCAATTTCCCATTCAGTATGACAAACATGCA	480
Db	421	CGAGGCCCCCTGGGGCATCATCACTCCGCCCAATTTCCCATTCAGTATGACAAACATGCA	480
Qy	481	CACGTGTGTGTGATCATCAGACACTCAACCCCTCCAAAGGTATCAAGCTCGCTTTGAG	540
Db	481	CACGTGTGTGTGATCATCAGACACTCAACCCCTCCAAAGGTATCAAGCTCGCTTTGAG	540
Qy	541	GAGTTGATTTGGAGAAGGGGCTATGACACCCCTGACGGTGGGATGGGTGACAGATGGG	600
Db	541	GAGTTGATTTGGAGAAGGGGCTATGACACCCCTGACGGTGGGATGGGTGACAGATGGG	600
Qy	601	GACCAAGAACAGATTCTCTACATGTCCTCAAAATGCTTCAGTGAACGCCCTCACACCCCA	660
Db	601	GACCAAGAACAGATTCTCTACATGTCCTCAAAATGCTTCAGTGAACGCCCTCACACCCCA	660
Qy	661	GGCTCTCCGATATCCAGAGAGCATGTCTGTGGGACATCTGAGAGCGAAATGGACTGTACTT	720
Db	661	GGCTCTCCGATATCCAGAGAGCATGTCTGTGGGACATCTGAGAGCGAAATGGACTGTACTT	720
Qy	721	GAGATCTGTGCTGACATTAGCAGTTCAATGCAAGTCAAGTTCAGTAGAGAAATCTTCCA	780
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Qy	781	AAAGCTTCTAATGCTGTGGAATTTGTTGCTCTGTGGACAAGATGAGACAGGGCATTTGC	840
Db	781	AAAGCTTCTAATGCTGTGGAATTTGTTGCTCTGTGGACAAGATGAGACAGGGCATTTGC	840
Qy	841	GGTGAACCCCTGGCATATCTGCATATGCGGAGGAAAGGCTCCCGTTTCAACAAGGTATAC	900
Db	841	GGTGAACCCCTGGCATATCTGCATATGCGGAGGAAAGGCTCCCGTTTCAACAAGGTATAC	900
Qy	901	ACACTCAAGTTTGAAGTGCACGCGCGCTTTTGAAGCTGTGTGGACAGAAAGGCATCATGTC	960
Db	901	ACACTCAAGTTTGAAGTGCACGCGCGCTTTTGAAGCTGTGTGGACAGAAAGGCATCATGTC	960
Qy	961	CAAAAGAAATAAACCAATGTGTGGCTTAAGAACCAAGGCTGTGTGTTCTCTGCTTCTTCAAC	1020
Db	961	CAAAAGAAATAAACCAATGTGTGGCTTAAGAACCAAGGCTGTGTGTTCTCTGCTTCTTCAAC	1020
Qy	1021	TTTCAACAGCCCTCTGAGGGTTGCTCTGTCTCCCACTACCCAGAGACATATGCGCAACAC	1080
Db	1021	TTTCAACAGCCCTCTGAGGGTTGCTCTGTCTCCCACTACCCAGAGACATATGCGCAACAC	1080
Qy	1081	CTTCACTGTGTCTGGCTCATCTCTGGCCAGGCTGAGAGCCGATCAACTGGCTTTCAAC	1140
Db	1081	CTTCACTGTGTCTGGCTCATCTCTGGCCAGGCTGAGAGCCGATCAACTGGCTTTCAAC	1140
Qy	1141	GACATTGACGTGAGGCTCAGTTTGAATTTCTGTGTCATCAAGATGGGGCCACCGCCGAG	1200
Db	1141	GACATTGACGTGAGGCTCAGTTTGAATTTCTGTGTCATCAAGATGGGGCCACCGCCGAG	1200
Qy	1201	GGGCGGCTCTGAGGACCTTCTCAAGAAACAGCTTCCCTCTCATCAACAAGCTGGC	1260

Db	1201	CGGCGCCGCTCGGGACACTTCTCAGAAACAGCTTCCTCTCATCACAAAGCAGTGGC	1260
Qy	1261	CACGTGGCCGCTCTCGAGTTCCAGACTGACCACTTCCACAGGAAAGAGGGCTTCAACATC	1320
Db	1261	CACGTGGCCGCTCTCGAGTTCCAGACTGACCACTTCCACAGGAAAGAGGGCTTCAACATC	1320
Qy	1321	ACTTTTACCACTTCCGACCAAGAGATGGCCGATCTGGCGTTTCCAGTAAATGCGAA	1380
Db	1321	ACTTTTACCACTTCCGACCAAGAGATGGCCGATCTGGCGTTTCCAGTAAATGCGAA	1380
Qy	1381	CGGTTTGGGGACAGCTTCAGCTGGGAGCTCCATCTTCCTTCTCTGTGATGAAGCTTC	1440
Db	1381	CGGTTTGGGGACAGCTTCAGCTGGGAGCTCCATCTTCCTTCTCTGTGATGAAGCTTC	1440
Qy	1441	CTTGGGATCTAGGGGCTCAGAGACATCACTCGGCTCCGTAAGAGAGGCGAGCGTGTG	1500
Db	1441	CTTGGGATCTAGGGGCTCAGAGACATCACTCGGCTCCGTAAGAGAGGCGAGCGTGTG	1500
Qy	1501	AACAGCGCTGTGCTCGGCTGTGAAGCTTCCCTGTGTGTGACCTGTACTTGGCCAGCGGC	1560
Db	1501	AACAGCGCTGTGCTCGGCTGTGAAGCTTCCCTGTGTGTGACCTGTACTTGGCCAGCGGC	1560
Qy	1561	ACCATCTCTCTCCGGGGCTGGGCTGGCTCTTACAAAGATGCTTGAAGCTGTGGCTGGGTG	1620
Db	1561	ACCATCTCTCTCCGGGGCTGGGCTGGCTCTTACAAAGATGCTTGAAGCTGTGGCTGGGTG	1620
Qy	1621	ATTGAGGCCACAGCGCTACCCCATCAAAATCACTTCGACAGATTCAAAACCGAGATC	1680
Db	1621	ATTGAGGCCACAGCGCTACCCCATCAAAATCACTTCGACAGATTCAAAACCGAGATC	1680
Qy	1681	AACTATGACACCTCTGGAAGTACGGGATGTGGGGACTTAATGAGGGCCCTTATGGGGTT	1740
Db	1681	AACTATGACACCTCTGGAAGTACGGGATGTGGGGACTTAATGAGGGCCCTTATGGGGTT	1740
Qy	1741	TACCAAGGAGCCACAGGTTCCCGAGTCCCTCATCGACACAGCAACTACTTACCTCTC	1800
Db	1741	TACCAAGGAGCCACAGGTTCCCGAGTCCCTCATCGACACAGCAACTACTTACCTCTC	1800
Qy	1801	TTCTCTACCGACAAAGATCACTCGGACATCGGGCTTCCAGCTCCGCTATGAGACTATTAACA	1860
Db	1801	TTCTCTACCGACAAAGATCACTCGGACATCGGGCTTCCAGCTCCGCTATGAGACTATTAACA	1860
Qy	1861	CTGCAAGTACAGCACTGTCTGGATTCAGAGATCCCAATTAATGACAGCGCTATGGGAAT	1920
Db	1861	CTGCAAGTACAGCACTGTCTGGATTCAGAGATCCCAATTAATGACAGCGCTATGGGAAT	1920
Qy	1921	GACTTCTACGATGGGCGCGCTGTGACCTTCACTGTGACTCTGGGCTACACTTAAGTGAC	1980
Db	1921	GACTTCTACGATGGGCGCGCTGTGACCTTCACTGTGACTCTGGGCTACACTTAAGTGAC	1980
Qy	1981	GGGAGGCTCTTGGATGTGAAGTGAAGCCCACTTCCAGTGGAGCGGGGCCCTGGCCAGTTGGA	2040
Db	1981	GGGAGGCTCTTGGATGTGAAGTGAAGCCCACTTCCAGTGGAGCGGGGCCCTGGCCAGTTGGA	2040
Qy	2041	GCTCTCTGTGGGCTTCAATCAAGGCTCCAGTGGGACATCTTGTGCGCAGGGTTCCCT	2100
Db	2041	GCTCTCTGTGGGCTTCAATCAAGGCTCCAGTGGGACATCTTGTGCGCAGGGTTCCCT	2100
Qy	2101	GACTTCTACCCCAACACTTGAATGTGACCTGTGATTAACGAAATCATCTCAGGCAAGGAT	2160
Db	2101	GACTTCTACCCCAACACTTGAATGTGACCTGTGATTAACGAAATCATCTCAGGCAAGGAT	2160
Qy	2161	GGTTCTTCACTTTCCACACCTTCCAGCTGGAAAGTGGCCATGTACTCTCTCATCT	2220
Db	2161	GGTTCTTCACTTTCCACACCTTCCAGCTGGAAAGTGGCCATGTACTCTCTCATCT	2220
Qy	2221	GAGAACGGACAGCTTACCCAGCGCCCTGAGGAGCTTAATCTGATCTCGGCTCCAGCTCC	2280
Db	2221	GAGAACGGACAGCTTACCCAGCGCCCTGAGGAGCTTAATCTGATCTCGGCTCCAGCTCC	2280
Qy	2281	ATCAGCGCTGGGCTTATGGAACCTTCACTGCCAGAGTCCGCTTCACTGATTTCTCC	2340
Db	2281	ATCAGCGCTGGGCTTATGGAACCTTCACTGCCAGAGTCCGCTTCACTGATTTCTCC	2340

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## ORIGIN

Query Match 86.0%; Score 8718.6; DB 9; Length 13113;  
Best Local Similarity 93.4%; Pred. No. 0;  
Matches 9389; Conservative 0; Mismatches 94; Indels 574; Gaps 4;

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 QY 5555 GGGGAGCTGGCTAACAGTGGGGAACAATGATGACTTGGAGTCCCGGGGATATCAAT 5614  
 Db 6433 GGGGAGCTGGCTAACAGTGGGGAACAATGATGACTTGGAGTCCCGGGGATATCAAT 6492  
 QY 5615 TGACTGGCAACCTGTCTCAAGTGTCAACATGGCAACAAACGGGAACCTGGGACCAACCCC 5674  
 Db 6493 TGACTGGCAACCTGTCTCAAGTGTCAACATGGCAACAAACGGGAACCTGGGACCAACCCC 6552  
 QY 5675 TGCCTAAGTGTGAAGTCCCTTGTGGCGGGAACATCACTTCTTCAACGGCACTGTGTACT 5734  
 Db 6553 TGCCTAAGTGTGAAGTCCCTTGTGGCGGGAACATCACTTCTTCAACGGCACTGTGTACT 6612  
 QY 5735 CCCCCGGGTTCCCTACCCGCTACTCAGCTCCAGAGCAAGTGTCTGAGTCAACCGTGC 5794  
 Db 6613 CCCCCGGGTTCCCTACCCGCTACTCAGCTCCAGAGCAAGTGTCTGAGTCAACCGTGC 6872  
 QY 5795 CCATTTGGCATGCGCTCCGCTCAACCTGAGCTGTGAGACAGAGCCCTCTGAGATT 5854  
 Db 6873 CCATTTGGCATGCGCTCCGCTCAACCTGAGCTGTGAGACAGAGCCCTCTGAGATT 6932  
 QY 5855 TCATTCACATCTGGGATGGGCGACAGCAAAACAGACCAAGGCTGCGCTTCAACCCGGA 5914  
 Db 6933 TCATTCACATCTGGGATGGGCGACAGCAAAACAGACCAAGGCTGCGCTTCAACCCGGA 6792  
 QY 5915 GCATGGCCAAAGAAAAAGTGCAGAGTTTCAATCAACCAAGGTTCTGCTCAAGTTCCACCGTG 5974

Db 6793 GCATGGCCAGAAAAAGTGCAGAGTTCATCCAAACAGGTCCTGCTCAAGTTCCACCGTG 6852  
 QY 5975 ATGCACCCCAAGGGGGGATCTTTCGCAATAGCTTTCCTGCTTATCCACTCCACCAATGCC 6034  
 Db 6853 ATGCACCCCAAGGGGGGATCTTTCGCAATAGCTTTCCTGCTTATCCACTCCACCAATGCC 6912  
 QY 6035 CTCCTCCCAACCATCTCTCCCAAGCGGCAAGTGGTCAAGAGATGAAGAAATTCATATAG 6094  
 Db 6913 CTCCTCCCAACCATCTCTCCCAAGCGGCAAGTGGTCAAGAGATGAAGAAATTCATATAG 6972  
 QY 6095 GTGACATGCTAGCGCTACAGATGCTCTCTGCTTTACTTTAGTGGGAATGAATTTCTGA 6154  
 Db 6973 GTGACATGCTAGCGCTACAGATGCTCTCTGCTTTACTTTAGTGGGAATGAATTTCTGA 7032  
 QY 6155 CCGCAAACTGGGAACCTACCTGCAATTTGAAGAACACCCCGAATATGTAAGTGCAT 6214  
 Db 7033 CCGCAAACTGGGAACCTACCTGCAATTTGAAGAACACCCCGAATATGTAAGTGCAT 7092  
 QY 6215 GTCCAACAATGAGCTTCTGACAGACTCCACAGGCGCTGATCCCTGAGCCAGACTACCTG 6274  
 Db 7093 GTCCAACAATGAGCTTCTGACAGACTCCACAGGCGCTGATCCCTGAGCCAGACTACCTG 7152  
 QY 6275 GAAAGCTATCCCAATGCTCCAGACTGCTTTGGCTGTGAGAGTGAAGCCGACTATACA 6334  
 Db 7153 GAAAGCTATCCCAATGCTCCAGACTGCTTTGGCTGTGAGAGTGAAGCCGACTATACA 7212  
 QY 6335 TCTCCCTCAGAGGAGTACTTCTGAGGAGAGAAATATGATGATTTGATTTTGG 6394  
 Db 7213 TCTCCCTCAGAGGAGTACTTCTGAGGAGAGAAATATGATGATTTGATTTTGG 7272  
 QY 6395 ATGCTTCATCAGAGAGAGTCTCTGCTGTAAGCCCTCAAGTGAATTACTCAGCTCCCG 6454  
 Db 7273 ATGCTTCATCAGAGAGAGTCTCTGCTGTAAGCCCTCAAGTGAATTACTCAGCTCCCG 7332  
 QY 6455 TGAATTTGTCACAGCTTCAAGCAACTCTGTGTACTGTGTGATCTGATCTGATCAAGCTTACA 6514  
 Db 7333 TGAATTTGTCACAGCTTCAAGCAACTCTGTGTACTGTGTGATCTGATCTGATCAAGCTTACA 7392  
 QY 6515 ATCGGAAGGGCTTCAAGATCCGCTATTTAGCCCTTACTGACGCTGACCGCCAGAGGCTCCAC 6574  
 Db 7393 ATCGGAAGGGCTTCAAGATCCGCTATTTAGCCCTTACTGACGCTGACCGCCAGAGGCTCCAC 7452  
 QY 6575 TCCATGAGCTTCACTTCAAGGCGAGACCAAGCCAGCCCGGGGCTTCATCTCACTTTGGCT 6634  
 Db 7453 TCCATGAGCTTCACTTCAAGGCGAGACCAAGCCAGCCCGGGGCTTCATCTCACTTTGGCT 7512  
 QY 6635 GCAAGCGCGGCTTACCGCTGTGGGAGACAGATGGCCATCTGTACCCGGACCCCGCAGG 6694  
 Db 7513 GCAAGCGCGGCTTACCGCTGTGGGAGACAGATGGCCATCTGTACCCGGACCCCGCAGG 7572  
 QY 6695 GCTACCACTGTGAGCGAAGCCATCCCTCTGTCAAGCTTTTCTGTGGGCTTCCG 6754  
 Db 7573 GCTACCACTGTGAGCGAAGCCATCCCTCTGTGTCAAGCTTTTCTGTGGGCTTCCG 7632  
 QY 6755 AGGCCCCCAAGATGGAATGTTGTGGCAAGAGTACAAGTGGGAACCAAGGCGCTGT 6814  
 Db 7633 AGGCCCCCAAGATGGAATGTTGTGGCAAGAGTACAAGTGGGAACCAAGGCGCAATGT 7692  
 QY 6815 AAGGCTGAGTGAAGGCTTACCACTCCAGGCGGCTGAGGCGCTGCAAGTGTCTGG 6874  
 Db 7693 AAGGCTGAGTGAAGGCTTACCACTCCAGGCGGCTGAGGCGCTGCAAGTGTCTGG 7752  
 QY 6875 ACACAGGCTTATGAGCAACCGCAATGTCACCAAGTGTGCTCTGATGATTTGCTCG 6934  
 Db 7753 ACACAGGCTTATGAGCAACCGCAATGTCACCAAGTGTGCTCTGATGATTTGCTCG 7812  
 QY 6935 ATGTGATGATGATCAAGCTGTGAGCATGGCCGATGAGAGGCTTATCTTTGAGACAGATATC 6994  
 Db 7813 ATGTGATGATGATCAAGCTGTGAGCATGGCCGATGAGAGGCTTATCTTTGAGACAGATATC 7872  
 QY 6995 AGTTCCAGGCGCGAGTATGCTATCTGTGACCTGCTGCTATCACTATCTGGCCAAAGG 7054

Db 7873 AGTTCCAGGCGCGAGTATGCTATCTGTGACCCCTGCTAGTACTATATCTGGCCAAAGG 7932  
 QY 7055 TCATCCGCTGTGAGGCGCAATGAGCAATGAGCTTGGGGAGCTTACGCCCACTGCCGAA 7114  
 Db 7933 TCATCCGCTGTGAGGCGCAATGAGCAATGAGCTTGGGGAGCTTACGCCCACTGCCGAA 7992  
 QY 7115 TCATCTCTGTGAGAGCTCCCGATTTCCCGCAATGGCCACCGCATGCGGAACACTGTCTG 7174  
 Db 7993 TCATCTCTGTGAGAGCTCCCGATTTCCCGCAATGGCCACCGCATGCGGAACACTGTCTG 8052  
 QY 7175 TCTACGGGCAACAGCCATCTTCTCTGCAATTCGATACACACTGTGTGGCTCCAGG 7234  
 Db 8053 TCTACGGGCAACAGCCATCTTCTCTGCAATTCGATACACACTGTGTGGCTCCAGG 8112  
 QY 7235 TGGCGATGATGAGCGCCAAATGGGCTCTGAGATGTGCTGGAATCCGCTGCTGTGAGC 7294  
 Db 8113 TGGCGATGATGAGCGCCAAATGGGCTCTGAGATGTGCTGGAATCCGCTGCTGTGAGC 8172  
 QY 7295 ACTGTGGACTCTGTAGGCCCATTTGTCAACGGACACATCATGGGAGAACTACACTACC 7354  
 Db 8173 ACTGTGGACTCTGTAGGCCCATTTGTCAACGGACACATCATGGGAGAACTACACTACC 8232  
 QY 7355 GGGGCAGTGTGTATCCATATGCAATGCTGCTTCCGCTGATGCGCATGTCTGTGCGCA 7414  
 Db 8233 GGGGCAGTGTGTATCCATATGCAATGCTGCTTCCGCTGATGCGCATGTCTGTGCGCA 8292  
 QY 7415 TCTGCACAGAGATCATCACTGTGTGGGCAAGCCCTTCTGTGTGCAATTACTGTG 7474  
 Db 8293 TCTGCACAGAGATCATCACTGTGTGGGCAAGCCCTTCTGTGTGCAATTACTGTG 8340  
 QY 7475 GACACCCAGGACCCCTGTCAACGGGCTCACTCAAGGATACCAATTAACCTCAACGATG 7534  
 Db 8341 GACACCCAGGACCCCTGTCAACGGGCTCACTCAAGGATACCAATTAACCTCAACGATG 8340  
 QY 7535 TGTGCAAGTTTGTTCACACCTGGGATATGCTGAGGGGGCTGTAGTCCCATGCC 7594  
 Db 8341 TGTGCAAGTTTGTTCACACCTGGGATATGCTGAGGGGGCTGTAGTCCCATGCC 8340  
 QY 7595 TGGCCAGCGGGCAATGAGATGACATGCTGCCACCTGAGAAATCATCACTGTACAGATC 7654  
 Db 8341 TGGCCAGCGGGCAATGAGATGACATGCTGCCACCTGAGAAATCATCACTGTACAGATC 8340  
 QY 7655 CTGACACCAAGAAAATAGTGTGTCAGTTCACAGCCAGCGGCCGACAGATTCACT 7714  
 Db 8341 CTGACACCAAGAAAATAGTGTGTCAGTTCACAGCCAGCGGCCGACAGATTCACT 8340  
 QY 7715 TCGGACCACTGTGTCTTACCGGTGACCAACAGGCTTCACTCTGTGGGACCCCACTGC 7774  
 Db 8341 TCGGACCACTGTGTCTTACCGGTGACCAACAGGCTTCACTCTGTGGGACCCCACTGC 8340  
 QY 7775 TCAAGCTGACAGGAGATGACATGAGACCGTCCCGCCCAAGTGTCTTGGTGTCT 7834  
 Db 8341 TCAAGCTGACAGGAGATGACATGAGACCGTCCCGCCCAAGTGTCTTGGTGTCT 8349  
 QY 7835 GTGGCCATCCGGGCTCCCGCTCACTCCAGATGTCTGAGACAGTTATATCTGTGGAG 7894  
 Db 8350 GTGGCCATCCGGGCTCCCGCTCACTCCAGATGTCTGAGACAGTTATATCTGTGGAG 8409  
 QY 7895 CAGTGTGCGGCTTACAGCTGATCGGCAAGCTATCTGTGTGGGAAACAGCACCCGCAATG 7954  
 Db 8410 CAGTGTGCGGCTTACAGCTGATCGGCAAGCTATCTGTGTGGGAAACAGCACCCGCAATG 8469  
 QY 7955 GTGGGCTGATGAGACACTGAGCTGGCTCCCTCTCACTGCTCAGGAACAGAGCTGGAG 8014  
 Db 8470 GTGGGCTGATGAGACACTGAGCTGGCTCCCTCTCACTGCTCAGGAACAGAGCTGGAG 8529  
 QY 8015 TTTCGGGTGACCTTGGGATTCGCGCTCATGTGCATTCGTTTGGGGAGAGCTTTGATCCAG 8074  
 Db 8530 TTTCGGGTGACCTTGGGATTCGCGCTCATGTGCATTCGTTTGGGGAGAGCTTTGATCCAG 8589  
 QY 8075 GCACTGTGATGCGGTTGAGCTGTGAAAGCTGCGCACGTTCTCCGGGATCTGTCAAGAGCGCA 8134  
 Db 8590 GCACTGTGATGCGGTTGAGCTGTGAAAGCTGCGCACGTTCTCCGGGATCTGTCAAGAGCGCA 8649





Db 1921 GACTTCTAGTGGGCGCTGGTGAACCTTACGTGTGACCTCGGGCTACACATTAAGTGAAC 1980  
 Qy 1981 GGGGAGCCTCTGTGAAGTGTGAACCCCACTTCCAGTGAAGCCGGGCTCTGCCAGTTGTGA 2040  
 Db 1981 GGGGAGCCTCTGTGAAGTGTGAACCCCACTTCCAGTGAAGCCGGGCTCTGCCAGTTGTGA 2040  
 Qy 2041 GCTCTCTGTGTGGCTTCAATTCAGAGGCTCAGTGGGACCATCTGTGGCCAGGGTCCCT 2100  
 Db 2041 GCTCTCTGTGTGGCTTCAATTCAGAGGCTCAGTGGGACCATCTGTGGCCAGGGTCCCT 2100  
 Qy 2101 GACTTCTACCCCAACAATTGAATCTGCACCTGTGATTTAGAAACATCTCATGGCAAGGT 2160  
 Db 2101 GACTTCTACCCCAACAATTGAATCTGCACCTGTGATTTAGAAACATCTCATGGCAAGGT 2160  
 Qy 2161 GTGTCTTCACTTTTCCACACTTTCACCTGTGAAGAGTGGGCACTAATCTCTCATCACT 2220  
 Db 2161 GTGTCTTCACTTTTCCACACTTTCACCTGTGAAGAGTGGGCACTAATCTCTCATCACT 2220  
 Qy 2221 GAGAAAGGAGCTTCAACCAAGCCCTGAGGAGCTAACTGATCTGGGCTGAGGCTGCC 2280  
 Db 2221 GAGAAAGGAGCTTCAACCAAGCCCTGAGGAGCTAACTGATCTGGGCTGAGGCTGCC 2280  
 Qy 2281 ATCAGGCTGGGCTCTATGGCACTTCACTGCGCAGGCTCGCTTCACTCTGATTTCTCC 2340  
 Db 2281 ATCAGGCTGGGCTCTATGGCACTTCACTGCGCAGGCTCGCTTCACTCTGATTTCTCC 2340  
 Qy 2341 ATGTCTATGAAGAGATTCAACATCACTTCTCAAGATGAGATTGGAAGCCCTGTGAGAG 2400  
 Db 2341 ATGTCTATGAAGAGATTCAACATCACTTCTCAAGATGAGATTGGAAGCCCTGTGAGAG 2400  
 Qy 2401 CCGGAGGCTCCAGCCTACAGCAATCCGGAAAGGCTTCAGTTGGGCTGGGCGCAACCTTG 2460  
 Db 2401 CCGGAGGCTCCAGCCTACAGCAATCCGGAAAGGCTTCAGTTGGGCTGGGCGCAACCTTG 2460  
 Qy 2461 ACCCTCTCTGCTTCCCGCGGATACCGTCTGAGAGGACCGCCGCACTCACTGCTGGGG 2520  
 Db 2461 ACCCTCTCTGCTTCCCGCGGATACCGTCTGAGAGGACCGCCGCACTCACTGCTGGGG 2520  
 Qy 2521 GGGCAGACGGGCTGTGAGAGCTGCTGTGCAAGGTGTGTGTGAGTGTGGAATTGA 2580  
 Db 2521 GGGCAGACGGGCTGTGAGAGCTGCTGTGCAAGGTGTGTGTGAGTGTGGAATTGA 2580  
 Qy 2581 GTCAAGGAGCTCAAGGCTCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
 Db 2581 GTCAAGGAGCTCAAGGCTCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
 Qy 2641 CATGATGATCTACTCCATCCAGACCCAGCCAGGAGGAAATTGAGTGAAGGCGAG 2700  
 Db 2641 CATGATGATCTACTCCATCCAGACCCAGCCAGGAGGAAATTGAGTGAAGGCGAG 2700  
 Qy 2701 GCATTCGAATCTCCGAGAGAGATGTCTCAAGTTTATGATGGAACAACAATCTCGCC 2760  
 Db 2701 GCATTCGAATCTCCGAGAGAGATGTCTCAAGTTTATGATGGAACAACAATCTCGCC 2760  
 Qy 2761 CGTTTGTGGAGTTTATGAGCAATCTGATGATGATGAGGAGTCTTGAACAGCAATCC 2820  
 Db 2761 CGTTTGTGGAGTTTATGAGCAATCTGATGATGATGAGGAGTCTTGAACAGCAATCC 2820  
 Qy 2821 ASCAGTGTGGCTGTGATTTCACTGATGCTGAAGAAACACAGCAAGGCTTTGAACGT 2880  
 Db 2821 ASCAGTGTGGCTGTGATTTCACTGATGCTGAAGAAACACAGCAAGGCTTTGAACGT 2880  
 Qy 2881 CACTTTTCCAGCTTTGAACCTCAATGATGAGAGCCAGGAAACCCCAAGTTTGGCTAC 2940  
 Db 2881 CACTTTTCCAGCTTTGAACCTCAATGATGAGAGCCAGGAAACCCCAAGTTTGGCTAC 2940  
 Qy 2941 AAGGTCATGATGAAGTCAATTTTGAAGGAGTCCGTGCTTCAAGCTGTGACCTGTGA 3000  
 Db 2941 AAGGTCATGATGAAGTCAATTTTGAAGGAGTCCGTGCTTCAAGCTGTGACCTGTGA 3000  
 Qy 3001 TACAGCTCGGGGTGATGAGAGTGTGTCTGATGAGAGGCGCGGACCTGGAGC 3060  
 Db 3001 TACAGCTCGGGGTGATGAGAGTGTGTCTGATGAGAGGCGCGGACCTGGAGC 3060

Db 3001 TACAGCTCGGGGTGATGAGAGTGTGTCTGATGAGAGGCGCGGACCTGGAGC 3060  
 Qy 3061 CGGCTCTGGCCCAACCTGTGTCCCGAGTGTGAAGGACAGTGAAGAGAGGTGTGGGG 3120  
 Db 3061 CGGCTCTGGCCCAACCTGTGTCCCGAGTGTGAAGGACAGTGAAGAGAGGTGTGGGG 3120  
 Qy 3121 CAGGTGTCTCAACCGGGATATCAGTCCCTATGAACAACAATCTCAATCTGTAACC 3180  
 Db 3121 CAGGTGTCTCAACCGGGATATCAGTCCCTATGAACAACAATCTCAATCTGTAACC 3180  
 Qy 3181 ATGAAAGCAGAGCGCGCTGACCAATTTGGCTTACATCTCTGTGTTGACAACAAGAG 3240  
 Db 3181 ATGAAAGCAGAGCGCGCTGACCAATTTGGCTTACATCTCTGTGTTGACAACAAGAG 3240  
 Qy 3241 GTTCAAGAGTGTGTGCAATCTGAGATGGGCTGTGAGAGAGGGGTTTGTGTAAGAG 3300  
 Db 3241 GTTCAAGAGTGTGTGCAATCTGAGATGGGCTGTGAGAGAGGGGTTTGTGTAAGAG 3300  
 Qy 3301 CTGAGTGGCCCGGCTGTGCAAGAGCTGATAGACCTTCAACTCGGTCTGTGAG 3360  
 Db 3301 CTGAGTGGCCCGGCTGTGCAAGAGCTGATAGACCTTCAACTCGGTCTGTGAG 3360  
 Qy 3361 TTCAAGACTGACTTCTTCAACAGCAAGAGGCTTTGCCATTTCAATTTCAATGTCACA 3420  
 Db 3361 TTCAAGACTGACTTCTTCAACAGCAAGAGGCTTTGCCATTTCAATTTCAATGTCACA 3420  
 Qy 3421 GCAAGTCTGTGAATGACCTGTGGATCCCGCAAGATGGAGTGTGAGTGTGACAGTTGG 3480  
 Db 3421 GCAAGTCTGTGAATGACCTGTGGATCCCGCAAGATGGAGTGTGAGTGTGACAGTTGG 3480  
 Qy 3481 GAAGCGGAGCTTCAACAGTGTTCAGTGTGACCTGTGATGAGGCTGTGAGGAGATGGA 3540  
 Db 3481 GAAGCGGAGCTTCAACAGTGTTCAGTGTGACCTGTGATGAGGCTGTGAGGAGATGGA 3540  
 Qy 3541 GAGATCAGCTGTGTGAAGATGAGAAACAGATTCTTGTGAGCCCAAGCCGCAACATGC 3600  
 Db 3541 GAGATCAGCTGTGTGAAGATGAGAAACAGATTCTTGTGAGCCCAAGCCGCAACATGC 3600  
 Qy 3601 ATCGCTCTGTGGGGGAGACCTTGAACAGACCATCTGAGTCACTCTTCAACCAATTAC 3660  
 Db 3601 ATCGCTCTGTGGGGGAGACCTTGAACAGACCATCTGAGTCACTCTTCAACCAATTAC 3660  
 Qy 3661 CCAGAAACCTTACCGGCAAGAGAGTGTGCTGGAAGTGAACCGTCTCACAGACTAC 3720  
 Db 3661 CCAGAAACCTTACCGGCAAGAGAGTGTGCTGGAAGTGAACCGTCTCACAGACTAC 3720  
 Qy 3721 GTCATGCGCCTGTGATTTAACAATCTTTAACAATCTGAGCCTGAGTATGACTTCTCATATC 3780  
 Db 3721 GTCATGCGCCTGTGATTTAACAATCTTTAACAATCTGAGCCTGAGTATGACTTCTCATATC 3780  
 Qy 3781 TACAGAGAGGAGACTTCTGAGCCTCTCATAGGAAGTCTTATGAGTCTCCAGCTCCA 3840  
 Db 3781 TACAGAGAGGAGACTTCTGAGCCTCTCATAGGAAGTCTTATGAGTCTCCAGCTCCA 3840  
 Qy 3841 GGCAGATTTGAAGAGAGCAACAGCCTCTTCTGAGCCTTCCGAGCAGATGATGTG 3900  
 Db 3841 GGCAGATTTGAAGAGAGCAACAGCCTCTTCTGAGCCTTCCGAGCAGATGATGTG 3900  
 Qy 3901 AGCAATGTGAGCTTGTCTATTAACAATCTTTAACAATCTGAGCCTGAGTATGATGATCT 3960  
 Db 3901 AGCAATGTGAGCTTGTCTATTAACAATCTTTAACAATCTGAGCCTGAGTATGATGATCT 3960  
 Qy 3961 GGTTCATTAAGAGAGGACAGGGTGTGGGCTTCCAGCTTGAAGTGTGGCTCTCCGACAC 4020  
 Db 3961 GGTTCATTAAGAGAGGACAGGGTGTGGGCTTCCAGCTTGAAGTGTGGCTCTCCGACAC 4020  
 Qy 4021 TACTACTGACAGGGGGCTTACGAAGTGAAGGACCTTGAACCTGAGCTGATCTCTGGGG 4080  
 Db 4021 TACTACTGACAGGGGGCTTACGAAGTGAAGGACCTTGAACCTGAGCTGATCTCTGGGG 4080  
 Qy 4081 CCTGATGGAGACCCGTGTGGAACAATCCCGGCAAGTGTGACAGGCCCCCTGTGGGGGA 4140  
 Db 4081 CCTGATGGAGACCCGTGTGGAACAATCCCGGCAAGTGTGACAGGCCCCCTGTGGGGGA 4140



QY	4141	CAGTATGTGGGTTCCGACGAGTGGTCTTGTCCCTCCCAATCACTCCCAAGTCAACAGT	4200
Db	4141	CAGTATGTGGGTTCCGACGAGTGGTCTTGTCCCTCCCAATCACTCCCAAGTCAACAGT	4200
QY	4201	GACAGATCTGCTGTATTTTGTACTGTGGCCAGAGCTATGTGTGTGTGGCCAGTTC	4260
Db	4201	GACAGATCTGCTGTATTTTGTACTGTGGCCAGAGCTATGTGTGTGTGGCCAGTTC	4260
QY	4261	GCCTTCTTTCACACGGCCCTCAACAGCGTGTGGAGGTTTCAAGACGAGCAGCAGAC	4320
Db	4261	GCCTTCTTTCACACGGCCCTCAACAGCGTGTGGAGGTTTCAAGACGAGCAGCAGAC	4320
QY	4321	TGGGGGCTCCTACGCTCCCTCTCGGGCTCCCATAGAGAAATCATGCTCTTGCCACC	4380
Db	4321	TGGGGGCTCCTACGCTCCCTCTCGGGCTCCCATAGAGAAATCATGCTCTTGCCACC	4380
QY	4381	TCCAAATCAAGTTCTCATTAAGTTACAGCGCCAAAGGCTCTCGACCGACGAGAGGTTTCAC	4440
Db	4381	TCCAAATCAAGTTCTCATTAAGTTACAGCGCCAAAGGCTCTCGACCGACGAGAGGTTTCAC	4440
QY	4441	TTTGTCTAACCAAGCGGTTCTCTGAAACAGCGCACGACGAGTCAAGTCTGTGCGCGAAACC	4500
Db	4441	TTTGTCTAACCAAGCGGTTCTCTGAAACAGCGCACGAGTCAAGTCTGTGCGCGAAACC	4500
QY	4501	CGCTATGGCAAGGGGTGGGGCAGTACATTCCTCGGTGGGGGCAATGTCCTTCGAAATGC	4560
Db	4501	CGCTATGGCAAGGGGTGGGGCAGTACATTCCTCGGTGGGGGCAATGTCCTTCGAAATGC	4560
QY	4561	AACTCCGGTATGCCCTCGAGGGGTCCGACAGATCGAGTGCCTCCCTGTGCTCGGGGCC	4620
Db	4561	AACTCCGGTATGCCCTCGAGGGGTCCGACAGATCGAGTGCCTCCCTGTGCTCGGGGCC	4620
QY	4621	TTGGGCCAAATGGAATGCTCAGCGGCCACGTGTGTGGTCCGTGTGAGGCAACTTCACA	4680
Db	4621	TTGGGCCAAATGGAATGCTCAGCGGCCACGTGTGTGGTCCGTGTGAGGCAACTTCACA	4680
QY	4681	GAGCGCAGGGGCAACATCTGTCCCTGGCTTCCAGACGCGTACCTCAACAGCTCAAC	4740
Db	4681	GAGCGCAGGGGCAACATCTGTCCCTGGCTTCCAGACGCGTACCTCAACAGCTCAAC	4740
QY	4741	TGTGTGTGGAAGATGTGGTGTCCCGAAGCGCTGGATCCAGATCCAAAGTTGTCAAGTTT	4800
Db	4741	TGTGTGTGGAAGATGTGGTGTCCCGAAGCGCTGGATCCAGATCCAAAGTTGTCAAGTTT	4800
QY	4801	GTCACAGACGAACTGGGACTCGCTGGAGATTTGATATGTGTCAAGATTAACATGTAAACC	4860
Db	4801	GTCACAGACGAACTGGGACTCGCTGGAGATTTGATATGTGTCAAGATTAACATGTAAACC	4860
QY	4861	ATGCTGGGAGTTCCTCAGAAACAACCGTGTGCTCCCTTGTGAACAGACCTTCAACAG	4920
Db	4861	ATGCTGGGAGTTCCTCAGAAACAACCGTGTGCTCCCTTGTGAACAGACCTTCAACAG	4920
QY	4921	CTCTAACCTTCATTTCTACTCAGATATCAGGCTATCTGACGTGGCTTCACTTGAAGTAC	4980
Db	4921	CTCTAACCTTCATTTCTACTCAGATATCAGGCTATCTGACGTGGCTTCACTTGAAGTAC	4980
QY	4981	AAAACGGTGGGCTGAGACATTTGTCGCGAATCCTGTGCTCCAGTAAACGGGGTGAAGACT	5040
Db	4981	AAAACGGTGGGCTGAGACATTTGTCGCGAATCCTGTGCTCCAGTAAACGGGGTGAAGACT	5040
QY	5041	GGCGAGCGCTACTTGTGGAAATGATGTGTGTCTTTCCAGTGTAGCCGGGATATGCTTC	5100
Db	5041	GGCGAGCGCTACTTGTGGAAATGATGTGTGTCTTTCCAGTGTAGCCGGGATATGCTTC	5100
QY	5101	CAGGGCCACGCCACATCTCTGTGATATGTGTGTCTTTCCAGTGTAGCCGGGATATGCTTC	5160
Db	5101	CAGGGCCACGCCACATCTCTGTGATATGTGTGTCTTTCCAGTGTAGCCGGGATATGCTTC	5160
QY	5161	CCAATCTGTATGACAGTGTGGGGGGAACAGTGAAGAGATGAGAGGGGTGATCTTGAGC	5220
Db	5161	CCAATCTGTATGACAGTGTGGGGGGAACAGTGAAGAGATGAGAGGGGTGATCTTGAGC	5220

QY	5221	CCGGGCTTCCCAAGCACTAACCCAGTAACATGACGTGCTCTGGAAAATAGACCTGCC	5287
Db	5221	CCGGGCTTCCCAAGCAACTAACCCAGTAACATGACGTGCTCTGGAAAATAGACCTGCC	5287
QY	5281	GTGGGCTTTGGAGCTCACATCCAGTTCCGAACTTCTCACCGAGCCCAACCAACGACTAC	5343
Db	5281	GTGGGCTTTGGAGCTCACATCCAGTTCTCGAACTTCTCACCGAGCCCAACCAACGACTAC	5343
QY	5341	ATTAGAAATCCGGAATGCGCCCTATGAGACAGCCGCGATGATGGAGAATTCAGTGGAAAGC	5400
Db	5341	ATTAGAAATCCGGAATGCGCCCTATGAGACAGCCGCGATGATGGAGAATTCAGTGGAAAGC	5400
QY	5401	GAGCTTCCAAAGCTCCCTCTCCACAGTCCCAAGACACACCGTATATTTCCACAGCCAC	5466
Db	5401	GAGCTTCCAAAGCTCCCTCTCTCCACAGTCCCAAGACACACCGTATATTTCCACAGCCAC	5466
QY	5461	CACCTCCAGAAATCGGCGAAGATTCAAGCTGAGATTCAGGCTATAGAACTTCAAGAGTGC	5520
Db	5461	CACCTCCAGAAATCGGCGAAGATTCAAGCTGAGATTCAGGCTATAGAACTTCAAGAGTGC	5520
QY	5521	CCAGAACCAAGACCCCTTTGGCAATGGCAATTTGTGAGGGGAGCTGGCTTACAGTGGACAA	5580
Db	5521	CCAGAACCAAGACCCCTTTGGCAATGGCAATTTGTGAGGGGAGCTGGCTTACAGTGGACAA	5580
QY	5581	TCAGTGAACCTTGAAGTGCCTCCGGGGATCAATTGACTGGCCACCCGTCTCAAGCTGT	5640
Db	5581	TCAGTGAACCTTGAAGTGCCTCCGGGGATCAATTGACTGGCCACCCGTCTCAAGCTGT	5640
QY	5641	CAACATGGGCAACCAATCGGAATGGGACACACCCCTGCGCAAGTGTGAAGTCCCTTGTGGC	5700
Db	5641	CAACATGGGCAACCAATCGGAATGGGACACACCCCTGCGCAAGTGTGAAGTCCCTTGTGGC	5700
QY	5701	GGGAACATCACTTTTCCAGGGCACTGTACTCCCGGGGTTCCCTAGCCGCTACTCC	5760
Db	5701	GGGAACATCACTTTTCCAGGGCACTGTACTCCCGGGGTTCCCTAGCCGCTACTCC	5760
QY	5761	AGCTCCCAAGA CTGTGTCTGGCTGATACCGTGGCCA TTGGCCATGGCGTCCGCTCAAC	5820
Db	5761	AGCTCCCAAGA CTGTGTCTGGCTGATACCGTGGCCA TTGGCCATGGCGTCCGCTCAAC	5820
QY	5821	CTCAGCCCTGCGAGACAGAGCCCTCTGGAGATTTCACACATCTGGGATGGGCCACAG	5880
Db	5821	CTCAGCCCTGCGAGACAGAGCCCTCTGGAGATTTCACACATCTGGGATGGGCCACAG	5880
QY	5881	CAAAACAGCAACGAGCTCGGCTCTTCCACCCGGAGCATGGCCAAAGAACAGTGCAGAGT	5940
Db	5881	CAAAACAGCAACGAGCTCGGCTCTTCCACCCGGAGCATGGCCAAAGAACAGTGCAGAGT	5940
QY	5941	TCATCCAAACAGGCTCTGCTCAAGTTCCACCGTGATGCACACAGGGGGGATCTTCGCC	6000
Db	5941	TCATCCAAACAGGCTCTGCTCAAGTTCCACCGTGATGCACACAGGGGGGATCTTCGCC	6000
QY	6001	ATAGCTTTCTCCGTTATTCACATCAACAAATGCCCTCTGCCACATCCGCCCAAGGCC	6060
Db	6001	ATAGCTTTCTCCGTTATTCACATCAACAAATGCCCTCTGCCACATCCGCCCAAGGCC	6060
QY	6061	GAACTGCTCACAGGAATGAAGAAATTCATATATAGTGACATCGTACGCTACAGATGCTTC	6120
Db	6061	GAACTGCTCACAGGAATGAAGAAATTCATATATAGTGACATCGTACGCTACAGATGCTTC	6120
QY	6121	CCTGGCTTTACCTTAGTGGGGAATGAAATTCTGACCTGCAAACTTGGAAACTTACCTGGAG	6180
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 Sun, P.C., Upadurai, R., Schmidt, A.P., Davis, M.E., Quant, E.C., Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B. Transcription map of the Bp23 putative tumor suppressor region Genomics 75 (1-3), 17-25 (2001)  
 JOURNAL MEDLINE 21365705  
 PUBMED 11472063  
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 Sun, P.C., Upadurai, R., Schmidt, A.P., Davis, M.E., Quant, E.C., Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B. Direct Submision Submitted (09-JAN-2001) Otolaryngology, Washington University School of Medicine, Box 8115, 517 S. Euclid Ave, Saint Louis, MO 63110, USA  
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2143 AATCTCAATGAGGAGGAGTGTCTTCACTTTCACACTTCACCTGGAAGTGGCAAT 2202  
3192 GTCTCTCATGSCAAGGAGTGAAGATGAAATTCACACTTCACCTTGAAGATTCACAC 3251  
2203 GACTACCTCTCATCTAGAGAACGAGCAGCTTCAACCCAGCCCTGAGGAGCACTGAATGGA 2262  
3252 GACTATTTGCTGATCAGAGAGATGGAGATTTCTCAGAGCCAGTGAAGCCAGCTCACTGG 3311  
2263 TCTCGGCTGCCAGCTCCATCAGCGCTGGGCTCTATGSCAATTCACCTGCGAGTCCGC 2322  
3312 TGAGTCTGCTCAGACCACTTAAGGCTGTGTGTGGAACCTTCACTGCAACACTCAGG 3371  
2323 TTCACTCTGATTTCTCCATGTCTATAGAGATTCACATCACTCTCCAGATGACAG 2382  
3372 TTCACTCTGACTTCTCCATCTCTATGAGGCTTCAACATTAAGTTGCAAAATATGAC 3431  
2383 TTGAGACCTGTGAGAGAGCCGAGGCTCCAGCTACAGCATCCGGAAGGCTTGAAGTT 2442  
3432 CTGAGACCTGTGATGATGACCTGGAATCCCTGCTTCAGCCGAGAAATGGTTTCAATTC 3491  
2443 GCGGTGGGAGCAACTTGAATCTTCTCTGCTTCCCGGATACGCTGTGAGGAGCAACCGC 2502  
3492 GGTGTGGGTGAGACCTGTGCTTTCACCTGCTTCAGGAGATACCGGTAGAAAGTCAAC 3551  
2503 GGCATCAGTGGCTGGGGGAGAGAGGCGCTGTGAGCTGCGCTGCGCAAGTGTGT 2562  
3552 AAGCTTACCTGCTGGGTGGGAGAGCGCGAGTGTGAGTCACTGTGCAAGTGTGTG 3611  
2563 GCTGAGTGTGGGAATTCAGTCAACAGCACTCAGGATCTTGTCTGCCCAACTTTTCT 2622  
3612 GGTGATGTGAGAGCAAGCTCAAGAGATGAGAAACATTAATCTCTCCAAATTTTCCA 3671  
2623 GTGAATCAATTAACATATGATGATGATCTCTCATCCATCCAGACCCAGCGAGAGGGA 2682  
3672 TCCCATTAATGATTAATACATAGTGTATCTTAATAATGAAACAGAGCCCGGAAAGGG 3731  
2683 ATTTCAGTGAAGCCAGGAGCTTCGAACTCTCGAAGAGATGTCTCTCAAGGTTTATGAT 2742  
3732 ATTCATCTGAGCTGAACTTCAGCTCTTCGAAAGAGACATCTTAAGGTTTATGAT 3791  
2743 GGCACAAACAACTCCGCGCTTGTGTGAGGATTTTGAAGCATTCGATGAGTGAAGGAG 2802  
3792 GGAAGAGAGAGCTCTCTCAAGTCACTGTGTGTCTTCAAGAGAGGAAATTCATGGGCTG 3851  
2803 ACTTGAACAGACATCCAGCAGTGTGTGTGATTTGATTCATCATGATGTGAAGAACACC 2862  
3852 GTGTCTCAACAGACCTCCAACTAGAGGCTGAGGTTCAACACCAACGGGTCGAGAACCC 3911  
2863 AACCAAGGCTTTGAATGCACTTTTCAGCTTTGAATCATCAATGTGAGAGAACCCAGGA 2922  
3912 GCCCAAGGCTTCCAGCTCACTCAACAGATTTTGACTAGTAAATGTAGGATCCAGGCG 3971

2923 AACCAGAGTTTGGCTACAGAGTTTCAATGATGAGATCAATTTTGCAGGAGCTCCGTGTC 2982  
3972 ATCCCTAATTAATGAGTACAGATCCGTGATGATGAGCCACTTCAACAGCACTGATGATCTC 4031  
2983 TTCACTGTGACCTCTGATTAACAGCTGTGGGGGTATGAGAGCTGTCTGTGTGATGGA 3042  
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3043 GAGCGCCGAGCTTGGGAGCCGAGCTCTGCGCACCTGTGTGCGCGAGTGTGAGAGGAGCA 3102  
4092 GAGCGAGGAGTGTGGAGCAAACTATGCTCTCTGTGTGTGAGTGTGTGTGTGTGT 4151  
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4152 CATGAGCCATCATCGGGCGCATACTGTCTCTGAGTACCCGCGCCATATGACAAACAC 4211  
3163 CTCACTGATCTGTGACATGAAAGCAGAGGCGGCTGACACATTTGGGCTTACCTTCTG 3222  
4212 CTTCAGCTGACCTTGAACATGAGGCGGATCTGGAAGACATCAAGCTTCAATTCAT 4271  
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4272 GTGTTTGAACATGAAGGCGCATGACATCTTCAAGGCTGTGGATGCTCTGTAGACAGC 4331  
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4332 AACATCTGTGAAGAGAGTGTGAGGCGGTTGCGCCCTTACTGAGACATCAGACACTTC 4391  
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4632 CCAAGCCTCTCTGTGTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4691  
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4692 ATTTATCTCCCAACTACCAACAGCATACCTCTCTGGAAGAGTGTGAGTGTGAGTGTG 4751  
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3763 TATGATCTCTCAATCTATCAAGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3822  
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3823 TATGCTCCAGCTTCCAGGCGGATTAAGAGCAGAGCAACAGCTTCTCTGCGCTTC 3882  
4872 CAGGCTCTCAAGCCCAAGAGAGTGTGAGAGAGTGTGTAACAGCTCTTCTGTGCAATTC 4931  
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3943 GAGTATGTTTGT 4002  
4992 GAGT 5051  
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 Qy 4063 CTGAGCTGATCTCTGGGGCTGATGAGAAAGCCGTGTGAAACAATCCGGGCAAGTCTGC 4122  
 Db 5112 ATTGAATGTGTGACAGGGGCTGATGAGAAAGCCGTCTGGGACCGGACACTACTGCTGC 5171  
 Qy 4123 AACAGCCCTGTGGGGGACAGTATGTGGGTGGAGAGAGTGTCTGTGCCCCCACTAC 4182  
 Db 5172 CAAGCACCCGTGTGAGGACAGTACACGGGCTCGAGGGGGTATTTTGTACCAAACTAC 5231  
 Qy 4183 CCCCAAGACTACACAGTGAAGACAGATCTGCTGTATTTTGTACTGCCCCAAGACTAT 4242  
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 Qy 6163 CTTGGAACCTACCTGAGTGTGAGAGCAACCCCGATATGTAAGTGAAGTGTGCAAG 6222  
 Db 7212 CTTGGAACCTACCTGAGTGTGAGAGCAACCCCGATATGTAAGTGAAGTGTGCAAG 7271

QY	6223	AATGACCTTCTGACAGACTCCACAGCCGATGATCTTGACCCAGACTCACTCCGAAAGCTAT	6282
Db	7272	AATGAAGTCGGAACAGAGCTCTTCTGGGGGTAATCTTCAGTCCCGGGTATCCAGGCAACATAT	7331
QY	6283	CCCCAGTTCCAGACCTGCTCTTGCGCTGGAGAGTGGAGCCCGCATTAATCACTGCCCCCTC	6342
Db	7332	TTTAACTCCAGACATGCTGCTTGGAGTATTTAAAGTGAACCAACTTCAACATCACTT	7391
QY	6343	ACAGTGGAGTACTTCTCAGCGAAGAACAAATGATGAGTTGAGATTTTGTATGCTCA	6402
Db	7392	TTTGTGGACACATTCGMAAGTAAAGCAATTGATGCACTGGAGTGTGATGATGCT	7451
QY	6403	TCAGGACAGAGTCCCTGCTGMAAGGCCCACTAGGGGAATTAATCAGTCCCCCTGATTTTC	6462
Db	7452	TCTGAGCGAAGTCTCTGTAGTGGTCTTAACTGGAAACCACTGMAACGTCCAAATTTT	7511
QY	6463	ACCAGCTCAAGCAACTGTGTATCTGCTGCTGGTGTGATCTGATCAAGCTCAATTCGAAAG	6522
Db	7512	ACCAGCAGAAAGTAACATCTGTAACTGTGCGCTGTGTCCAGACCAATGACACAGCAAGAA	7571
QY	6523	GGCTTCAAATCCGCTATTCAAGCCCCCTTATCTGACGCTGGCCCCAGGGCTTCACCTCCATGGC	6582
Db	7572	GGATTTCMAATTCGCTATGTACAGCTCTTACTGCAACCTCACCTCTACACTCAGAAATGCT	7631
QY	6583	TTCATCTTACGGCAGACAGCAAGCCAGCCCGGGGCTCCATCACTTTGGCTGCAAGCC	6642
Db	7632	GGCATTTTAAATAAAAACGCTGTGGGCACTTGGAGAACAGTACATTACTTCTGCAAGCTT	7691
QY	6643	GGCTACCGCTGTGGGGAACACAGATGGCCATCTGTACCCGGACACCCCAAGGGCTAACAC	6702
Db	7692	GGATATTCGAATGATTGGCCACAGCAATGGACCTGACGGCGGAACCCAGTGGGGTGTAT	7751
QY	6703	CTGTGAGCGGAAGCCATCCCTTCTCTGTCAAGTCTTCTGTGGGCTTCTGAGGCCCCC	6762
Db	7752	CAGTGGGATTCGATGGCACCACTTTTGGCAGGCTGTGTCTGTGMAATTCAGAGGCTCCG	7811
QY	6763	AAGAATGGAATGGTGTTTGGCAAGAGTACACAGTGGGAAACCAAGGCCGTGTACAGCTGC	6822
Db	7812	GGAAATGGCTATTCACGGGGCAATAGTTCACCTTAAAGACATTAAGTAAATGAT	7871
QY	6823	AGTGAAGCTTACCACTCCAGGGCAGCGCTGAAGCCACTGCAAGGTCTTGAACACAGCC	6882
Db	7872	AATGAAGGCTTTCMACTGGATGCGAGTCAAGAAAGCCACCACTGTATGTCAGAAAGATGGC	7931
QY	6883	CTATGAGAGCAACCGAATGTCCACACAGAGTGTCCCTGTGACCTTGTCTGATGTCAGT	6942
Db	7932	CTGTGAGACACAGAAAGCCACATGCAAAACCGGTGCCCTGCCCCAGCATGAA	7991
QY	6943	AGCATCAGCGTGGAGACATGGCCGATGAGAGGCTTATCTTTGAGACACAGTACATTTCCAG	7002
Db	7992	GGCAGCTGTGAGACAGTGTGTCTGGAAGGCTGGTTCGGGATCACTGAATGAATTAAGGA	8051
QY	7003	GGCCAGCTGATGCTATCTGTGAACCTCTGGCTACTATTACTGSCCAAAGGGTCATCGC	7062
Db	8052	GCTCAAGTCTCTCCTCAGCTGCAAGCCCCCGCTACTTCTTGACGGGTTCAGAGGCTCTTGACG	8111
QY	7063	TGTCAGCGCAATGGCAAAATGAGAGCTGGGGGACTTACGCCCACTGCCAATCATCTCC	7122
Db	8112	TGTCAGCGCAATGGGACTTGAAGCACTGAGGAAGACAGCCCAATGTAAGATCATCTCC	8171
QY	7123	TGTGGAAGCTCCCGATTTCCCCCAATGGCCACCGCATCGGAACACTGTCTGTCTACGGG	7182
Db	8172	TGTGGAAGCTGTCTCTTCCCCCAATGTGTAACAAATAGGAAGCTCACTAATTAACGA	8231
QY	7183	GCAAGAGCATTTCTCTGCAATTCGGAATACACACTGTGGGCTCCAGGGTGTGAG	7242
Db	8232	GCACTGTGCATCTTAACTGTGAATTAAGGTCTACACTTGTGGGCTCCACAGTCCGGAG	8291
QY	7243	TGCATGGCAATGGGCTCTGGAGTGGCTGTGAAGTCGCGCTTGCGTGAACACTGTGGG	7302
Db	8292	TGCTTGGCAATGTGCTCTGGAATGGATCAAGAAACAAAGTGTCTGGCGGGCATTTGGCGC	8351

QY	7303	ACCTCCGAGCCCAATTGTCAAGGACACATCAATGAGGAGAACTAAGCTACCGGGGACGT	7363
Db	8352	TCTCCAGACCCCAATTGTGATAGCCATATACCGGGTAGTGGTTTCAAGCTACAGAGACACA	8411
QY	7363	GTGGTGTACCAATGGCAATGCTGGCTTCGGCTGATCGGACATGTCTGTGGCATCTGGCAG	7422
Db	8412	GTGGTGTACCAATGGCAACCTTGAGTTCCGGGCTCGTGGGACCTCTGTGGAATTTGG - CTG	8470
QY	7423	CAGGATCATCACTGGTTCGGGAGAGC - CCTTTCTGTGTGCCAATTACTGTGGACACCC	7483
Db	8471	CAGGACCAACATGTGTGGGGGAGACTACTGTGTGTGTCCCAACATGATGGACACC	8530
QY	7483	AGGCAACCTGTCAACCGGCTCTACAGAGGTAAACAGTTTAACTCAACGATGTGTGCA	7541
Db	8531	TGGAAACCCTGGCCCATGGGCTTCCAAAGGACACGAGTTCAACTGGAACACCTTGTGA	8590
QY	7542	GTTTGTATTGCAACCTGGGATATGGTCTGAAGGGGCTCTAGTCCCATGCTGGCCAG	7601
Db	8591	TTTCACTGGCCATCTGGCTACCGGCTGACGGGTGGCTTCCGAGCCCATGTTCGAGGCA	8655
QY	7602	CGGGCAATGGAAGTGCATGCTGCCACCTGGACAAATCAACTGTACAGATCCCGGCA	7663
Db	8651	CGGCCAGTGGAGACGCCCTTGGCCATGTTCGAGTGAACGTTCGACCCCGGATC	8710
QY	7663	CCAGAAAAATAGTGTTCGTCAAGTTCACAGCCAGCGGCCCGCACAGTTCAGCTTCGACAC	7721
Db	8711	TGTGAAAAATGCAAGTTCGCCCATGGGCAACAGAACTTTCCAGAGATTTGAGTATGGAC	8770
QY	7722	CACCTGTCTTAACCGGTGCAACACAGGCTTTACTCTCTGGGACCCCAAGTCTCACTG	7781
Db	8771	AGTGTGATGTATCACTGCAAAACGGGGTTTACTTGTGGAGTCTTCTGCTCGAAGCTG	8830
QY	7782	CCAGGAGATGGCAATGGACCGTCCCGGCCCATAGTCTCTTGGTGTCTGTGGCCA	7841
Db	8831	CATGGCAAGTGGCTGTGGGACCGGCTCTTACCAAGTGTGTGGCTATATCATGTGGGCA	8890
QY	7842	TCCGGGCTCCCGGCTCACTCCCAAGTCTTGGAGACATTTATCTGGGAGCATGTGCT	7901
Db	8891	TCTCTGGGCTCCCTGTATATGCTGTCTGACATGGAGAAATGTTTCAATCGAGGACACGCT	8950
QY	7902	GGGGTACAGCTGCATCGGCAAGCGATCTGTGGGAAACAGCAACCGCATGTGGGGCT	7961
Db	8951	TCAGTACTCTCGCAAAAGGGGGCCAGATCTCAAGGCAACAGCAACAGATCTGCCAAGA	9010
QY	7962	GGATGACATGGAAGTGGCTCCCTCTCACTGCTCAGGAAACAGCGTGGAGTTTGGCG	8021
Db	9011	AGACAGTCACTGAGTGGATCCCTTCTCATTTGTTCAGAAATAGTCCGTGATTTTGGG	9070
QY	8022	TGACCCCTGGGATCCCGGCTCATATGCAATCCGTTTGGGGAGCAGCTTGTATCCAGGCACTGT	8081
Db	9071	TGATTCAGGGACCCGACACATGGGCTCTGCTTGGGAGATGATTTAAGAACAAAGATCT	9130
QY	8082	GATGGCTTCAAGCTGTGAAGCTGGCCACAGTGTCCGGGGATCTGCAAGAGCGCATCTGTCA	8141
Db	9131	TTTGGGCTTCTCTGTGATAGGGCCACAGCTGGGGGCTTTGCAAGACGCAATGCTCT	9190
QY	8142	AGCCATATGGCTGTGGAGCGGCTGCGAGCTGATGTGGAGTATCTCTTGTGGAAACC	8201
Db	9191	GGTAATATGATCTCGGTCAAGAGATTAAGCCTGTGTGAGAGCCGTGTCTCGCGGAAACC	9250
QY	8202	TGGGACTCAAGTATATGCGGAGTTGGTTCAAGATAGGCTGGTTTCTCCAGCTCAT	8261
Db	9251	AGGCAACGCGACCAAGGGAGATCTTCAGCAGTGAATGGATCTCTTCTCCAGCTCTGT	9310
QY	8262	CGTCTATAGTGCAGGAAAGGATTACTACGCCACAGGCTGTCAAGCCGTCACTGCTCGGT	8321
Db	9311	CATCTATAGCTGTGGAAAGGCTTACAAGACGTGGGGCTCATGCTCGGCACTGCACGGC	9370
QY	8322	CAATGTATCTCGGACAGGCAAGTACCTTGAATGTCTGTATTAACGTGTGGTACCTCTGG	8381
Db	9371	CAATGTGACGTGGACAGGCAAGTCTCTGTGCTGACAAATATCAAGCTGTGGGATCTCTGG	9430
QY	8382	GATTCAGGCATATGGCTTGGGCTGGGCAATGACTTGAAGTACAAACAACTGTGACATA	8441





126 CAATGACATCTGGAATGAT-TACTCATGACGAGACCCAGTCCAGGGTAAGCAATTCCAG 184  
QY 2689 CTGAAGCCGAGGCGATTCGAACTCTCCGAGAGAGATGCTCTCAAGGTTATGATGCAAC 2748  
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 DB 1558 TGTCAAGAGTTTCAAGAGAGCGCTCGCTGTGAGAGACACAGGCCCATCTGCCAGAG 1617  
 QY 400 CCGATGTGTATGCCCCACCTTGAGAGCCCCCTGCGGATCATCACTCCCAATTTCC 459  
 DB 1618 AGAACTATGATGATCAATCTGTGGTGGGCCAAGGGGTATTAATCTCCCTTAATTAATCCG 1677  
 QY 460 ATTCAATATGACAAATATCAATCACTGTGTGTGATATATCAAGCACTCAACCTCCCAAG 519  
 DB 1678 GTTCAGTATGAAGATATATGACACATGTGTGTGTATCATCACACACACCCGGAAG 1737  
 QY 520 GTGATCAAGCTCGCCCTTTGAGAGGTTGATTTGAGAGGGGCTATGACACCCCTGACGG 579  
 DB 1738 GTCACTCAAGCTTGCCCTTTAAGAGTTTGAAGCTGAGAGCGGCTATGACACCCCTGACGG 1797  
 QY 580 GGTGATGTGTCAAGATGGGAGCCAGAAAGAGAGTCTCTACATGTCTCAAAATGCTGAC 639  
 DB 1798 GGTGATGTGGGAAAGGTGGAGACACAGATCGGTCTGTAGCTG-----1842  
 QY 640 AGTGACAGCCCTCAACCCCAAGGCTCTGCAATCCAGAGAGCATGTCTGGGAGCATTTGG 699  
 DB 1843 -----CTACGGGATTCAGTGTCTGACCTCAT--TGTGAGCATGAGC 1884  
 QY 700 AGCAGAAATGGAAGTGTACTTGAATCTGTGCGTACATTAGCAGATTGATGCAAGATCA 759  
 DB 1885 AACCAATGTGCTACATCTGCAATGCGATGATGATGATGCT-----1927  
 QY 760 GGTTCAGTAGAAGTCTTCAAAAGCTTCTAAATGTGTGTGAACTTGTGCTCTGGAGCA 819  
 DB 1928 -----CACCTGGGTTTAAAGCTTTTAAACAA 1953  
 QY 820 GAGATCGACAGGCGAGTGGCGGTGACCTTGGCATATCTGCAATATGCGCGAGGAAAGGC 879  
 DB 1954 GAAATTTGAAAAGGAGGGGTGGGATCTCTGGAATCCCGCTATGAGGAAGCGAGCGGC 2013  
 QY 880 TCCCGGTTTCAACGAGTGACACTCAAGTTTGAAGTGCAGCCGCTTTGAGGTGAGTGG 939  
 DB 2014 AGCAGTTTCTCTCAATGAGATACACTCACTTTGATATGCCCGGCGCTTTGAGTGGAGT 2073  
 QY 940 GGCAGAGAGGCAATCAATGCCAAAAGATTAACAATGTGTGCTTGAAGAGCAGAGCTGC 999  
 DB 2074 GGGAGAGAGTATATCACTGCTGAGGAGAAATATGAGTGTCTGGACAAGCCAGCTGT 2133  
 QY 1000 GTGTTCTCTGCTTCTTCACTTCAACAGCCCGTCTGGGGTGTCTGTCTTCCCACTAC 1059

DB 2134 GTATTTTCATGTTTCTCACTTACGGCATCATCTGGGATTAATCTGTCAACCAATTAT 2193  
 QY 1060 CCAAGGACTATGGAACCACTCTCACTGTGTGTGCTCATCTCGGCAAGGCTTAGAGC 1119  
 DB 2194 CCAAGGATATGGAACCAATGAACGTGTGTGTGATTAATCTCGAGGCAAGAGT 2253  
 QY 1120 CGCATCACTGGGCTTCAACGACATGACGTGAGGCTCAGTTGATTTCTCGGTCTATC 1179  
 DB 2254 CGAATTCACCTTAATCTTAAATGATTTGATGTGAGCTCAATTTGACTTTCTCGCGGT 2313  
 QY 1180 AAGATGGGCGACCGCGGAGCGCCGCTCTGCGGACCTTCTCAGAAACAGCTTCC 1239  
 DB 2314 AAGATGATGACATTTCTGATTAATCTGTCTCGGGTACTTTTCTGCGAAATGAGTGCT 2373  
 QY 1240 TCTTCATCAAGAGAGGCGACAGTGCCGCTCTGAGTTCAGACTGACATCTCCACA 1299  
 DB 2374 TCCAGCTGCGCAGAGGCGCATATATGTTGCTTGGAAATTCAGTGTGACATTTCCACT 2433  
 QY 1300 GGGAAAGGGGCTTCAACATCACTTTTACACCTTCCAGACAAAGAGTGCCTGATCCT 1359  
 DB 2434 ACTGGCAGAGGTTTCAATCATCTTACACCACTTTGTGATGATGATGCTGCATGATCT 2493  
 QY 1360 GCGCTTCAATTAATGCAAAAGGTTGGGAGACAGCTTCCAGCTGGGCACTTCATCTCC 1419  
 DB 2494 GGCATTCCTATTAACGAGACGATTTGTGTGACAGGTTTCTAATCGGAGCTCGGTTTCT 2553  
 QY 1420 TTCCCTGTGATGAAGGCTTCTTGGGACTCAGGGCTCAGAGCATCACTGCGCTCTG 1479  
 DB 2554 TTCACTGTGATGATGCTTTGTGTAAGCCAGGAGATCGAGTCAATCACTGCACTAG 2613  
 QY 1480 AAGAGGCGACGCTGTGTAACAGCGCTGTGCTGCGGTGTAAGCTCCCTGTGTGTGT 1539  
 DB 2614 CAAGCGGAAAGTGTGTGAGGCTCAACGCTGCCGCTGTGAAGCTCAATGTGTGGA 2673  
 QY 1540 CACTGACTTGGCCAGCGGACCATCTCTCTCGGGCTGGCTGCTTCAAGAT 1599  
 DB 2674 CATCTGAGAGGTCCAGGAGTCAATTTGTGCTCTGATGCGCAGATATTAATGAGAT 2733  
 QY 1600 GCCTTGAAGCTGTGCTGGGTGATTTGAGGCGCAGGCTACCCCATCAAAATCACTTC 1659  
 DB 2734 TCTTTACATTTGATGATTAATGAAACAAACAGGCCACTTATCAAAATGACTTTT 2793  
 QY 1660 GACAGATTCAAAACGAGTCAACTATGACACCCCTGGAAGTACGATGCGGAGCTTAC 1719  
 DB 2794 GACAGATTTCAGACAGAGTCAATTAATGACACTTTGAGGTCAAGATGGCCAGCCAGT 2853  
 QY 1720 TCAAGCGCTTGTATGCGGTTTACAGGGAGCCAGGTTCCCACTTCTATACAGACC 1779  
 DB 2854 TCGTCCCACTGATCGGAGTACCAAGGACCCAGGACCCCAAGTCTCTATCAGCACCC 2913  
 QY 1780 AGCAACTACCTCTACCTCTCTCTTCTTACCGCAAGAGTCACTGAGCATGGGCTTCCAG 1839  
 DB 2914 GGGAACTTATATGATGAGGCTTGAATCGGATTCCTGCTGAGCCCGGATCCCTGTG 2973  
 QY 1840 CTCGCTATGAGACTATTAACCTGCACTGACAGCACTGTCTGATTCAGAAATCCAGTA 1899  
 DB 2974 ATTCACATATGAGATGAGGCTTGAATCGGATTCCTGCTGAGCCCGGATCCCTGTG 3033  
 QY 1900 AATGACAGGCTCATGGGAATGATTTCTAGTGGCGCGCTGTGATCTTCACTGTGAC 1959  
 DB 3034 AACGGCCATGCGCACGGTGAAGATTTGGATCAAGGTTCACAGTCACTTTCAGCTGTGAC 3093  
 QY 1960 TCGGGCTACACATTAAGTGAAGGAGGAGGAGCTGTGAGTGTGAGCCCACTTCAGTGGAGC 2019  
 DB 3094 CCGGGGTACACATTAAGTGAAGGAGGAGGAGGCTGTGTGTGAGAGAAACACCAATGGAGC 3153  
 QY 2020 CGGGCCCTGCGCAATTTGAGCTCTGTGTGTGCTTCAATTCAGGCTCCAGTGGAGCC 2079  
 DB 3154 CAGGCTTGGCCAGCTGAGAGGCTCTATGTGAGAGTCAATTCAGAGGAAAGAGTGAACA 3213  
 QY 2080 ATCTTGTGCGAGGCTTCTGACTTCTACCCCAACATTTGAATGCACTGCAATTAATC 2139  
 DB 3214 GTCTTTCTCTGTGGTTTCCAGATTTTATCCAAACCTCTAAATGTCAGAGTGAACATTT 3273

OY	2110	GAACATCTCAATGGCAAGGATGTGTTCTTCCATCTTCCACACCTTCCACCTGGAAGTGGC	2159
Db	3214	GAAGTGTCTCAATGGGAAGAAGTTCAAAATGATCTTTCACACCTTTCATCTTGAAGTTC	3333
OY	2200	CATGACTACTCTTCATCATCTGAGAACCGGACGTTCAACCCAGCCCTTGAGGACACTAACT	2259
Db	3334	CACGACTATTTACTGATCATCAGAGGATGGAAATTTTTTCCAGCCCGTTGCCAGGCTCAC	3393
OY	2260	GGATTCGGGCTGGCAGCTCCCATCAGCGCTGGGCTCTATGGCACTTCACTGGCCAGGTC	2319
Db	3394	GGGTGGATGTGGCCATACGATCAAGGACAGGCCGTGTGGAAACTTCACTACGCCAAGCTT	3453
OY	2330	CGCTTCATCTCGATATTTCTCCATGTCATATGAAAGATTCAATCACTCACTTCTCAAGATAC	2379
Db	3454	CGGTTATATTCAGACTTCTCAATTTCTATCAGAGGCTCTCAATATCACTTTCAGAAATAT	3513
OY	2380	GACTTGGAGCCCTGTGAGAGCCGAGGTCCCAAGCTTACAGCATTCGGAGAGGCTTGCAG	2439
Db	3514	GACCTGGAGGACATGATGATATCTTGAAATCCCTGCTTCAACCGGAAGAAATGGTTTTAC	3573
OY	2440	TTTGGCGTGGGCGAACACTTGAACCTTCTCTCCGTCCCTCCGGGTACCGCTGGAAGGCAC	2499
Db	3574	TTTGGTGTGGGAGATCTCTGACGTTTTCTGCTTCTGGAATATCGTTTGAAGATGCC	3633
OY	2500	GCCCCATCAGGTGCTGGGGGGCGAGACGGGCGCTGTGAGAGCTGCGCTCTGCCAAGGTGT	2559
Db	3634	ACCAAGCTTACCTGCTGGGTGGGGGCGCGGTGTGTGGAATGACACTCTGCCAAGGTGT	3693
OY	2560	GTTGCTGATGTGGGAATTCAGTCAAGGACTCAGGGTACTTGTCTGTCCCCCACTTT	2619
Db	3694	GTTGGCGGATGTGGGCAAGGTGTCCAAAGAAATGAAAGAACTTACTGTCTCCAAATTTT	3753
OY	2620	CCTGGAACCTTCAATTAACATCATGATATCTATCTCCATCCAGACCAGCCAGGGAG	2679
Db	3754	CCATCCATTTATGATTAATACCATGATGATATCTTAATAATGAACAGAAAGCCGGCAG	3813
OY	2660	GGAATTCAGCTGAAAAGCAGGGGCACTTGAACCTCTCCGAAGAGATGTCCTCAAGTTTTAT	2739
Db	3814	GGCATCTCACCTTGAACACAGAAAGCTTTCAGCTGTTTGAAGAGATATCTTAAAGTATAT	3873
OY	2740	GATGGCAACAACAATCCGCCCGCTTGTGTGGAGATTTTAACCAATCTGAAATGATGGGG	2799
Db	3874	GATGGAAAAGACAGTTCTCTCAAGTCCATCTGGGACGTTCACTAAAGAACTTCTGGGG	3933
OY	2800	GTCATTTGGAACAGCACATCCAGCAGCTGTGGCTTGAATTCATCACTGATGCTGAAAAC	2859
Db	3934	CTGATCTCAACAGACATCCAAATCACTGTGGCTAAGATTTCAACCAATGATCTGAC	3993
OY	2860	ACCAAGCAAGGCTTTGAACTGCACTTTTCCAGCTTTGAACCTCATCAAAATGTGAGACCA	2919
Db	3994	ACCGACCAAGGTTTTTCAACTCACTCATACAGTTTTGATCTGTAATAATGAGAGATCCG	4053
OY	2920	GAAACCCCAAGTTTGGCTCAAGGTTATATGAAAGTCATTTTGACGGGAGCTCGGTG	2979
Db	4054	GGCATCTCTTAATCAGCGCTATATGGAATCCGTATGAAAGCCACTTATCCGACACTGTAAAT	4113
OY	2980	TCTCTCAGCTGTGACCTTGATATACAGCTCGGGGTATGTAGAGACTGTGTCTGAGT	3039
Db	4114	CTGTATCAATTTGCAACCCGGGGATCGCANTGACATGGACAAACCTCTGACTGTTTTGAT	4173
OY	3040	GGAAGAGCCCGGACCTGGGACCGGCTTGTCCACTGTGTGCGCGAATGTGAGGGGACA	3099
Db	4174	GGAGACAGAGAGTGTGGGAAACAACCACTTCTGTGTCATATGCGGAATGTGTGGTCCAG	4233
OY	3100	GTCAGAGAGAGATGTCCGGGCGAGGTGCTGTCAACCCGGGTATCCAGCTCCTATGAACAC	3159
Db	4234	ATCCATGACAGCAATACAGAGCAATATTTGTTCCTGTGCTATCAGCTCCGTAATGACAA	4293
OY	3160	AATCTCAACTGCATTTGGAACCATGAGCAAGAGCGCGCTGCACCATTTGGGCTTCACTTC	3219
Db	4294	AACCTCCACTGCACTGTGATTAATAGGACAGACCCAGGAAGAAAGACCATTTAGCTCCATTTCC	4353

OY	3220	CTGGGTTTGAACAAGAGAGATTACAGACGTGCTGGCAATCTGSGAATGGGCTGTGGAG	3279
Db	4354	ATTGTTTTCGACAGGAGATAGCTCAGACATCTCTCAAGGCTCTGGAGCGGCGGTGAC	4413
OY	3280	AGCGGGGTTCTGCTGAAGAGACTGAGTGCCCGGCGCTGCCAAGAGACTTCATAGCAC	3339
Db	4414	AGTGACATCTGTGGAAGAGATGGAGTGCGCTCGCGCTTCCGAGGACATCCACAGCAC	4473
OY	3340	TTCAACTCGGTGTCCTGCAAGTTACGACCTGACTTTCTTACACAGCAAGCAGGCTTTGCC	3399
Db	4474	TTCAACTCACTCACCTCTGACAGTGTGACAGCAGCATTTCTTCAACAGCATGTGCGCTTCC	4533
OY	3400	ATTCAATTTTGAAGTCCACAGCAACGTCCTGCAATGACCCCTGGGATCCGCAATGGG	3459
Db	4534	ATCCAGTTCTCACTCTCAATTGACAGCACCTGTAAACGATCAGGATATGCCCAAAATGGC	4593
OY	3460	AGTCGAGATGGTGAACATTTGGGAAAGCCGGCCACTCCACATGTTCCAGTGTGACCTTGAC	3519
Db	4594	AOCCTATGAGACAGCAGAGAGGCTGAGAACACCGTCACATTTCCAGTGTGACCTTGCC	4653
OY	3520	TACGCGCTGACAGGGAAGTGACAGATCAGCTGTGTAAAGATCGAACAAGTTCTTCTGG	3579
Db	4654	TATCAGCTCCAAAGACAAGCAAAATCACTGTGTGACGTGAATTAACCGGTTCTTTTGG	4713
OY	3580	CAGCCCAAGCCCCCAACATGATGGCTCCCTCGGGGGAACCTGACAGACCAATCTTGA	3639
Db	4714	CAACCAAGACCTCTTCACTCATGTATAGCTGTGTGAGGGAATCTGAACGGGCCACAGGT	4773
OY	3640	GTGATCTCTACCAAAATTAACCAAGACCTTACCCGACGAGCAAGATGTGACTGANA	3699
Db	4774	GTTATTTTGTCAACCACTTACCCACAGCCGATCTCTCTGGGAAGGAATGTGACTGAGA	4833
OY	3700	GTGACCGTCTGACCAAGACTAGCATGCGCCCTGTGATTTAAACATCTTTAACTTGAAGCT	3759
Db	4834	GTAAGAAGTAACCCGGAATTTGTGATGCGCTTGATTAATTAAGGATTTCAACATGAGAGCC	4893
OY	3760	GGCTATGACTTCTTCATATCTACAGCGAGCGGACTCTCTACGCTCTTATAGGAAC	3819
Db	4894	AGCTATGACTTCTTACATCATTAAGAAAGGGAATTTCCAAACAGCCCTCATTTGGGAGT	4953
OY	3820	TTCTATGGCTCCACGCTCCACAGGCGCATTAAGAACAGACGACAGCTCTTCTCGCC	3879
Db	4954	TACACGGGCTCTCAGGCCCCGAAAGATAGAGTAGCGAACAAGCTGTCTTGCA	5013
OY	3880	TTCCGACAGATGATCTGTAGCAATGCTGGCTTGCTATTTGACTATACAGAAAACCG	3939
Db	5014	TTTCGAGTATGCTCCGCTGGGCTTTACAGGTTCCGCAATGAATTAAGAGAAACCA	5073
OY	3940	CGGAGTCATGTTTGTGATCTGTTCATCAACAAAGCGCACAGGGTGGGCTCCGACCTG	3999
Db	5074	CGGGAAGCTTGTTTGACCCAGGAATTAATGATGGGACAAAGTTGGAACAGACTTC	5133
OY	4000	AAAGCTGGGCTCTCTCGTCACTTACTACGTGCAAGGGGCTTACGAATTTGAGGCACTCG	4059
Db	5134	AAAGTTGGCTCACCATATCACTTACAGTGAATCTGTGCTATTAAGATTTTGAACCTCTCA	5193
OY	4060	AACCTGAGCTGATCTCTGGGCGCTGATGAGGAAGCCGCTGTGGAACAATATCCCGGCGACTG	4119
Db	5194	TCATACACTGTGTGATGTGGGGCTGATGGGAAACCTCTGTGGACCAAGTGTGCTCTCC	5253
OY	4120	TGCAACGCCCCCTGTGGGGGACAGTATGTGGGTTCCGACGGAATGTCTTGTCTCCCAAC	4179
Db	5254	TGCAATGTCTCTGTGGAGGCAAGTACACGGGATCAAGAAAGGGATTAAGTTTATCAACAAAC	5313
OY	4180	TACCCCAAGAACTACACCAAGTGAACAGATCTGCTTTGATTTTGTATCTGTGCCAAGAC	4239
Db	5314	TACCCCAATAATTAACAAGCTGTCAATAATGCTCTATTTCAACACAGGTATCCAAAGAA	5373
OY	4240	TATGTGTGTTTGGCAGTGTGGCTCTTTTACACAGGCGCTCAACGACGTGTGAGAGTT	4299
Db	5374	TTCTGTGTCTTTGGACAGTTGTTGCTATTTTCCAGACAGCGCTTGATATGATTTTGGCAATTA	5433
OY	4300	CACGACGGCACAGGCAGCACTGCGGCTCTCAAGTCTCTTCTGGGCTCCCATACGA	4359







QY 6517 CGAAGGGCTTCAAGATCCGCTATTGAGCCCTTACTGAGCCTGCGCCAGGGCTCCACTC 6576  
DB 7654 AAGAAAGATTCAAGATTGGCTATTGACACCTTACTGAGTTGACCAACCCCTGAAG 7713  
QY 6577 CATGCTTATCTTAGGCGACAGCAGCAGCCCGGGGGCTCCATCCACTTTGGCTGC 6636  
DB 7714 AATGGGGGATTCTTAACAGGACTGAGGAGCGGTGGAAAGCAAAATGACTTATTTTTCG 7773  
QY 6637 AACCGCGCTACCGCTGGTGGAGACAGATAGGCGATCTGTACCCGGGACCCCGGAGGGC 6696  
DB 7774 AAGCTTGGAATCCGAATGGTGGCCACAGCATGCAACCTGTAGAGAAACCCACTTGGC 7833  
QY 6697 TACCACTGTGAGCGAAGCCATCCCTCTGTCAAGCTCTTCTGTGGGCTTCTGTAG 6756  
DB 7834 ATGTACCAATGGGACTCCCTCAAGCAGCTTGGCAGGCTGTCTGTGAATCCAGAA 7893  
QY 6757 GCGCCCAAGATGGAATGGTGTGGCGAAGAGTACAGATGGAAACAAAGCCGTGTAC 6816  
DB 7894 TCCCCAGAAACGGTTCATTACCGGGAAAGAGTTCACTTGGACAGTAAAGTGTCTAT 7953  
QY 6817 AGCTGAGTGAAGGCTTACCACTTCCAGGAGGCTGAGGCGCTGCAAGTGTCTGAC 6876  
DB 7954 GAATGTCATGAAAGCTTCAAGCTTGAATCCAGCAGACAGCAACCGCTGTCTCAAGAA 8013  
QY 6877 ACAGGCTATGAGAGACCGCAATGTCCACACAGTGTGCTGCTGTGACTTCTGTAT 6936  
DB 8014 GATGGCTGTGAGTAAACAAAGGGAAGCCGCCATGTGTAGCCGCTGTGCCCCAGC 8073  
QY 6937 GTCAATGATCAGCAGCTGAGCATGAGCCGATGAGAGCTTATCTTTGACACAGTATCAG 6996  
DB 8074 ATTGAAGTCAAGCTTCAGAAATGATCATCTGAGAGCTGTTCAGGATCTTTGAATGAG 8133  
QY 6997 TTCCAGGCGCAAGTATGTCTATCTGTGACCTGCTGCTACTACTGTGCGCAAGGGTC 7056  
DB 8134 TACGGTCTCAAGTATGTGAGCTCAAGCTGCTGCTGTACTACTTGAAGGCTGAGAGCTC 8193  
QY 7057 ATCCGCTGACAGGCAATGAGCAATGAGGCTGAGGAGCTCTAGCGCCACCTGCGAATC 7116  
DB 8194 CTGCGGTGCGAGGCAATGAGGAGCTGAGACATGAGAGTGAAGGCGCAAGCTTCCAGTT 8253  
QY 7117 ATCTCTGTGAGAGCTCCGATTTCCCGCAATGAGCAGCGCATCGGAACACTGTCTGTC 7176  
DB 8254 ATCTGTGTGGAAGCCTTCTCTTCCCGCAATGAGCAAAATGGAAGCTTGAACAGTT 8313  
QY 7177 TACGGGCGCAAGCCATCTTCTCTGCAATTCGGAATACACTGTGGGCTTCAAGGGTC 7236  
DB 8314 TATGGGGCGCAAGCTATATTACGTGCAACACCGGCTACACGCTGTGGGGTCTCATGTC 8373  
QY 7237 CGTGAATGATGAGCAATGAGGCTCTGAGAGGCTCTGAAGTCCGCTGCTGTGAGAC 7296  
DB 8374 AAGGAATGCTTGGCAATGAGGCTCTGAGAGGCGAGGAACCTGAATGTCTGGCTGCGAC 8433  
QY 7297 TGTGGAATCTTAGAGCCATTTCTCAAGGACACATCAATAGGAGAACTACAGCTACCG 7356  
DB 8434 TGGGTTTCCCGAAGCCGATTTGGAAGGTCATTAAGTGAATGGCTTCACTTACAG 8493  
QY 7357 GGCAGTGTGTGATCAATGCAATGCTGCTTCCGCTGATCGGCAATGTCTGTGCGCATC 7416  
DB 8494 GACACGCTGTGATCAAGTGCATCTGCTTCCGCTGTGGGAATCTTCCGTAAGAGATA 8553  
QY 7417 TGGCAGAGGATATCACTGTGGGCAAGACCCCTTCTGTGTCATTAATTAATCTGAG 7476  
DB 8554 TGGCTCAAGACCAAGTGTGTGAGCAAGCCGCTGTGTCTTCCCATCAATGTGTGT 8613  
QY 7477 CACCCAGGCAACCTGTCAAGGCTCACTCAGGGTAAACAGTTTAACTCAACGATGTG 7536  
DB 8614 CACCTTGAAACCTGCGCCAGGATTTCAATGAGAGTGTCAACCTGATGATGTC 8673  
QY 7537 GTCAAGTTGTGTCACCTGTGATATGAGCTGAGGGGCTGTAGTCTCCAAATGCTG 7596  
DB 8674 GTGAATTTCACTGCAACAGGGGCTATTGTGCTGAGGGGCTGTCTGAGGCCAGTGTGCG 8733

QY 7597 GCCAGGGCAATGAGTGAATGCTGCCCCACCTGAGAAATCATCACTGTACAGATCCT 7656  
DB 8734 AAGCAAGGCGCAATGAGTGAATCCCTGTGCCCAAGTGTGAGTGAATCTGTATCA 8793  
QY 7657 GGAACCAAGAAATATGTGTGTGTCAGGTCACGCCAGGGGCGGACAGGTTCACTTC 7716  
DB 8794 GGGTTGTGAAATATGCAATGTGTGTCAGGGCAACAGAACTTCCGTGAGGTTTGTGAT 8853  
QY 7717 GGCACACTGTGTCTTACCGGTCACACAGGCTTCTACCTCGGGGACCCAGGTC 7776  
DB 8854 GGAATGATATCTGTACCATTTGCAAGAGGATTTCACTTCTGAGATCTTCAAGCTTG 8913  
QY 7777 AGCTGCAAGGAGATGCAATGAGACCGTCCCGCCCAAGTGTCTTGTGTCTGT 7836  
DB 8914 ACTGTATGGAATATGCTTATGGAGCGATCCCTGCGCAAGTGTGTGCTATATCTGT 8973  
QY 7837 GGCATCCGGGCTCCCGCTCACTTCCAGATGTCTGAGACAGTTATCTGTGGAGCA 7896  
DB 8974 GGAACCCAGGGGATCTGCGCAAGCCGCTCTCACTGAGAGCTGTTCCTATGCGCC 9033  
QY 7897 GTGTGCGGTACAGCTGATGAGCAAGGCTACTGTGTGGAAACAGCACCCGCAATGTGT 7956  
DB 9034 GTGTGACTACTCTGCAAGAGGAGCGAGAGCTTATGAGCAAGAGATGTGTC 9093  
QY 7957 GGGCTGATGACACTGAGCTGAGCTCCCTCCCTCACTGTCTAGGAAACAGCGTGGAGTT 8016  
DB 9094 CAGGAAGACATGATCTGAGACGGGAGCTGCCCACTGCAAGAAATATCTGTGATTC 9153  
QY 8017 TCGGTGACCTTGGGATCCCGCTCAATGAGCATCCGTTGGGGACAGCTTTGATCCAGC 8076  
DB 9154 TGTGTGATCCGGGGAGCCCAAGCATGAGGTCTGCGCTTGTGTGATGATCTTTAAGAACAA 9213  
QY 8077 ACTGTATGCGGCTTACGCTGTGAGCTGAGCTGAGCTGAGGAGATCGTCAAGGCGAC 8136  
DB 9214 AGCTTCTCGCTTCTCTGTAAATGAGGACACAGTGAAGGCTCCCTGAAAGCAGC 9273  
QY 8137 TGTCAAGCAATGAGCTGCTGAGAGGCTGAGAGCTGAGTGTGAGTATCTTGTGG 8196  
DB 9274 TGTGTGCTCAATGAGGTCATGTGAGAGCTGAGAGCTGAGAGGCTGTGTGCTGTGCG 9333  
QY 8197 AACCTGAGACTTCAAGTATATCCGAGTGTGTCTGATGAGCTGTGTTTCTCAGC 8256  
DB 9334 AACCTGAGACACCAACCAAGGAATGATGTGATGATGAGGCAATCTGTCTCAGC 9393  
QY 8257 TCTATGCTATGAGTGTGCGGAGAGATCTACGCCAGGCTGTGACCGCTCACTGC 8316  
DB 9394 TCGGTATATGAGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 9453  
QY 8317 TCGGTCAATGATACCTGAGCAGGAGTACCTGAGTGTGCTGCTATTAATGTGGTAC 8376  
DB 9454 ACAGGCAATGAGACTGAGCAGGAGCTGCTCCGAGTGCACAAATTAATGTTGGGAT 9513  
QY 8377 CCTGGATTCAGGCAATGAGGCTTGGCTGAGCAATGACTTCAAGTAACTGAGTGTG 8436  
DB 9514 CCAGGCACTGAGCAATGAGGCTTCCAGTTTGGAGCCGACTTCAACAAAGTGTG 9573  
QY 8437 ACATATCAATGTGTCTCTGCTATATGATGAGTCAATAGATATCTGTGAGCTGC 8496  
DB 9574 ACTTATCAATGTGATCCAGGCTATGATGAGAGGCTCAATCCGCACTATTCGCTGT 9633  
QY 8497 ACCAAGGACCGGACATGAAATGAAACCAAGCCGCTGCAAGGCTCTCATGTGCAAGCA 8556  
DB 9634 ACCAAGGACCGGAGTGTGAAATCCGAGCAACCTGTGTGAAAGCCGCTGTGTCTCAG 9693  
QY 8557 CCTCGCTATCCCAATGGAAGGTGTGTGAGTGTGACTTCAATGTGAGTGTG 8616  
DB 9694 CCGCGCGCGTGAAGATGGAACAGTGAAGGAAAGTATTTCCGCTGGGGCTTCAAGCATA 9753  
QY 8617 ACTTATGCTGCTGAGAGGATACAGCTCTCTGCGCGGCTGTTCACCTGTGAGGAA 8676  
DB 9754 AGTTATGCTGATGAGAGGTTTACAGCTCTCTCACTTCCGCAATCTTCTCTGTGAAGGT 9813  
QY 8677 AATGGGTCTGAGACCGGAGAGCTGCTCAGTGTTCCTGTGTCTGCGGGGATCTGTGT 8736

Db 9814 CCGGGGGTGGAGAAAGAGAGATCCCCAGTGTCTCCCTGTGTCTGGGAGACCCCTGCG 9873  
 Qy 8737 GTCCCTCCCGGGGAGAGAGAGACCGAGGCTTCTCTACAGGTCATCTCTCTTC 8796  
 Db 9874 ATCCCGGAGAAAGGGGAGCTAGTGGAAAAAGTTTCACTATTAAGTCCAGATCTTCTTC 9933  
 Qy 8797 TCCCTGCAATCCCTCTGTGTGTGGGCTCTCAAGCAGGTTTGGCAGTCAATGAG 8856  
 Db 9934 CAGTGAATCTTCATTTATCTCTGTGGATCTCCAGAAAGTCTGCCAAGTGAAGGC 9993  
 Qy 8857 ACATGAGTGGACCCAGCCAGCTGATAGATCCAGCCCTGACCAAGTGTGGAGCCCT 8916  
 Db 9994 AGGTGAGGGGAGTAAACCAACCCAGTGTATCTGTCTATTAACCACTGCCCAAGCCCT 10053  
 Qy 8917 GGTGTGCCACAGTTGGGATACAGAACATTTCTCAGGGCTTACAGTTTGAAGCAGATC 8976  
 Db 10054 GGTACGCCACACTTGGAAATACAGAAATGCTCCAGAGGCTATGAGGTTGAAAGCAGGTT 10113  
 Qy 8977 CTCTCCGTTGTCAAAAAGGCTACTGTTCAAGGGCTCCAGCAGCAGACCTGCCCTCCA 9036  
 Db 10114 TTTTTCAGGTGAGAAAGGCTATTCATTAAGGTTTCCAGCACTGCACTGCTTGGC 10173  
 Qy 9037 AACCTGACCTGAGTGAACCCCACTGACTGTGTCTCCCACTGACAGCAGCCAGAG 9096  
 Db 10174 AATTTAACATGAGTGGATACAGACCAATGATATCTCATGCTGACAGCAGCCAGAA 10233  
 Qy 9097 AGGCCAAGCAGTCCCAAGCTCGGGGCTGATTTGCCCTCCATGGGCTCAACGCTCAT- 9155  
 Db 10234 ACCCGGGCAGACGGGATGTGAGAGCATGATCTTCTCACTTGGCTGACCTTAAGT 10293  
 Qy 9156 TACTCTGCGCAGAGAGGGCTTCTCCCTCAAGGGTGGCTCGAGACCGCAGCTGCAAGGG 9215  
 Db 10294 TACACTGCGCATTCAGGCTTTTCTCGAGGGGATCTGACAGCAAGAACATGTAAAGA 10353  
 Qy 9216 GATGCACTGAGACAGCAGCCGCCATCTGCTGAGAGTCCGGCCAGTGGAGACCC 9275  
 Db 10354 GACATGAATGAGCAGGAAAGTCCGCTGTGT-----GTAAAGTAA 10395  
 Qy 9276 ATCAACACTGCCCGGAGGACCCGCTCACCCAAAGCTTATTTCTGGGATGTTTTGGC 9335  
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 Qy 9336 AAGAAATCCCTGTGAAAGGGCTTATGATATCAAGGGAGAGAGACAGCCAGCTGCTC 9395  
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 Qy 9396 AAGTGACTGCTTCCAACTTGCACACAGCAAGTCAATGCCACATGATGACACAGT 9455  
 Db 10516 ACTGTTGACTGTTCAATGCAACAGCAAGTAAAGTAAAGCACCCTTCAGGAAAGCTCG 10575  
 Qy 9456 GGGGTGGAAGTCACTGTGCTGGAACCTTCAAGAAAGAGATTTTCTACTCTCCAG 9515  
 Db 10576 CCAAGTGAAGTAAAGTTGACAGGCATTTTCAAGAAAGAGAGAGCCCACTTACTGAAA 10635  
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 VERSION AX374893.1 GI:19169788  
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 ORGANISM  
 Rattus rattus (black rat)  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE  
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 Weicher, A.A. and Elliott, G.S.  
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 Amgen Inc. (US)  
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## ORIGIN

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REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Welcher, A.A. and Elliott, G.S.  
C3b/i4b complement receptor-1-like molecules and uses thereof  
Patent: WO 0210199-A 1 07-FEB-2002;  
Amgen Inc. (US)

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## ORIGIN

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Matches 6001; Conservative 5; Mismatches 3136; Indels 25; Gaps 3;

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Db 408 AGAATTTGAAAAGGAGGAGTGGGAGATCTTGAAATCCCGCTATAGGAAGCGGAGCGG 467

Qy 879 CTCCCGTTTACACGAGTGAACACTCAAGTTTGAAGTGCAGCCCGCTTTGAAGTGT 938

Db 468 CAGAGTTTCTTCATGAGATGATACATCACTTGAATGCCGCGCTTTGAAGTGT 527

Qy 939 GAGACAGAGCAATACATGCTCCAAAAGATACCAATGTGCTGCTAAGAAAGCCAGCTG 998

Db 528 GGGGAGAGAGATTATCACTGTGACAGAAACATCAGTGTGTGCAACAAGCCAGCTG 587

Qy 999 CGTGTCTCCGCTTCTTCACTTCAACAGCCGCTGAGGAGTGTCTGTCTCCCACTA 1058

Db 588 TGTATTTCAATGTTCTTCACTTTAGCGATCACTGAGATTAATCTGTACCAAAATTA 647

Qy 1059 CCCAGAGACTATGAGCAACCACTTCACTGTGTCTGCTCACTCTGCGCAGGCTGAGAG 1118

Db 648 TCCAGAGAAATATGGAACAACATGACTGTGTGCTGATTAATCTGAGCAAGAGAG 707

Qy 1119 CCGCATCACTGCGCTTCAACGACATGAGAGTGAAGCTCAAGTTGATTTCTCGTCAAT 1118

Db 708 TCGAATTCACCTAATCTTTAATGATTTGATGTTGAGCTCAATTTGACTTTCTCGCGGT 767

Qy 1119 CAAGATGGGGGCAACCGCGAGGCGCGCTCTGAGGCACTTCTCAGGAACAGCTTCC 1238

Db 768 CAAGATATATGCAATTTTGTGACATAACTGTCTTGAGTACTTTTCTGCGCAATGAGTCC 827

Qy 1239 CTCTTCATCAACAGAGCTGCGCAAGTGGCCCGCTTCTGAGTTCCAGACTGACACTCCAC 1298

Db 828 TTCCAGAGTGGCGAGCAATGAGCAATATAGTTCTGCTGAAATTTAGTGTGACATTTCCAC 887

Qy 1299 AGGGAAGAGGGGCTTCAACATCACTTTTACCACTTCCGACACAAAGAGTCCCGGATCC 1358

Db 888 TACTGCAGAGGGTCAACATCACTTAACACCACTTTGGTCAGAAATGAGTGCATATCC 947  
1359 TGGCGTCCAGTAATAAGGCAACGGTTTGGGAGACGCTTCAGCTGGGAGCTCCATCTC 1418  
948 TGGCATCTCTATAAAGGACGAGCTTTTGGTGAAGATTCTACTGGGAGCTCGGTTTC 1007  
1419 CTTCCTGTGATGAGGCTCTCTGGAACTCAGGGGTGAGAACCATCACTCGGCTC 1478  
1008 TTTCACCTGTGATGATGGCTTTTGTCAAGACCCAGGGATCCGATCCATTACCTGCATACT 1067  
1479 GAAGAGGAGCAGCGGTGTGAAACAGCGCTGTGCTGCGTGTGAAGCTCCCTGTGTGG 1538  
1068 GCAAGACGGGAAGTGGTCTGAGCTCCACCGTCCCGCTGTGAAGCTCAATGTGTGG 1127  
1539 TCACCTGACTTGGCCCAAGCGGACCATCTCTCTCCGGGTGGCTGGCTTCTCAAGGA 1598  
1128 ACATCTGACAGCGCTCCAGCGGAGTCATTTTGGCTCTCTGATGGCCAGGATATTAAGGA 1187  
1599 TGGCTTGAGCTGTCGCGGGTGAATGAGGCCAGCGGCTACCCCATCAAAATCACTT 1658  
1188 TTCTTTACATTGTAATGATTAATGAAGCAAAACAGGCACTTATCAAAATTAATCTT 1247  
1659 CGACAGATTCAAAACGAGGTCAACTATGACACCTGGAAGTAAGGATGGGCGGACTTA 1718  
1248 TGAACATTTCAACAGAGGTCAATTATGACACTTGGAGGTCAAGATGGGCGACCGAG 1307  
1719 CTCAGCGCCCTTGATGGGGTTTACACAGGAGCCAGGTTCCCGAGTTCTCATCAGAC 1778  
1308 TTGCTCCCACTGATCGGCGAGTACACAGGACCCAGGCACTCCATCTCTCATCAGAC 1367  
1779 CAGCACTACCTTACTCTCTCTCTCTCAACGCAAGAGTCACTCGGACATGGGCTTCCA 1838  
1368 CGGAACCTTATGATCTGCTATATTCACACTGACACAGCGCTTCAAGCATCGGCTTCT 1427  
1839 GCTCCGCTATGAGACTATAACACTGAGTCAAGCACTGTGTGATTCAGGAATCCAGT 1898  
1428 CATCCACTATGAGAGTGTGACGTTGATGCGATTTCTGCTGGAACCGGCGCATCCCTGT 1487  
1899 AATGAGCAGCGCTGATGGGAATGACTTCTAAGTGGCGCGCTGTGACCTTCACTGTGA 1958  
1488 GAACGCAATCGCCACGATGGGAATTTGGCATCAGGTCCACAGTGACTTCACTGTGA 1547  
1959 CTCGGGCTACACTTAAGTGAAGGAGCGCTCTGAGTGTGAAGCCCACTTCCAGTGTGA 2018  
1548 CCGGGGTACACTAAGTGAAGCAGACCGCTCTGTGTGAAGGAACCAAGTGTGA 1607  
2019 CCGGGCCCTGGCCAGTTGTGAAGCTCTGTGTGGCTTCACTCAAGGCTCCAGTGGAGC 2078  
1608 CCAAGCTTGGCCAGCTGCGACGCTCTATGTGAAGGTACATCAAGGGAAGAGTGAAC 1667  
2079 CATCTTGTGCGCAGGGTCCCTGACTTCAACCCCAAACTTGAAGTCACTGTGAATTA 2138  
1668 AGTCTTTTCTCGGGTTCAGATTTTATTCAAACTCTCTAAACGCGACGTTGACAT 1727  
2139 CGAAATCTCATGAGGAGGTGTCTTCACTTTCACACTTTCACACTGTGAAGTGG 2198  
1728 TGAAGTCTCATGAGGGAAGAGATTCAAAATCTTTCACACTTTCATTTAGAGTTC 1787  
2199 CCATGACTACCTCTCATCTAGAGAACGAGCACTTCAACCCAGCCCTGAGGAGTAAAC 2258  
1788 CCAAGACTATTTATGATATCAAGAGATGGAAGTTTTCGAGCCCGCTTCCAGGCTCAC 1847  
2259 TGGATCTGGCTGCGCAGCTCCATCAGCGCTGGGCTTATGAGCACTTCACTGCGCAGT 2318  
1848 CCGGTGCGGTGTCTCTCATATGAGTCAAGGAGCGCTGTTGGAACCTTCACTGCCAGCT 1907  
2319 CCGCTTCACTCTGATTTTCTCATATGATATGAAGATTAACATCACTTCTCAAGTA 2378  
1908 TCGGTTATATACAGACTTCTCAATTTCTGACGAGGGCTTCAATATCAATTTTCAAAATA 1967  
2379 CGACTTGAAGCCCTGTGAGAGCCGAGGTCCAGGCTACAGCATCCGGAAGGCTTGA 2438

Db 1968 TGAACCTGAGACCATGATGATATCTGAGTCCCTGCTTCAGCGGAAGATTGTTTCA 2027  
2439 GTTTGGCGGGGCGACACCTTGAACCTTCTCTGCTTCCCGGGTACCGTGGAGGCGAC 2498  
2028 CTTTGTGTGGAGACTCTGACGTTTCTCTGCTTCTGGGATATCTTTGAAGGTGC 2087  
2499 CGCCGCATACAGTGTGGGGGGGAGACGAGCGCTGTGAAGCTCGCTCTGCAAGTGG 2558  
2088 CACCAAGCTTACTGCTGCTGGGTGGGGCCGCGTGTGTGAAGTGAACCTCTGCAAGTGG 2147  
2559 TGTGTGAGTGTGGAATTCAGTCAAGGCACTCAGGGTACTTGTCTCCCAACTT 2618  
2148 TGTGGCCGAATGTGAGCAAGTGTCAAGGAATGAAGAACTTACTGTCTCAAAATT 2207  
2619 TCTGTGAATCAATAAATCAATATGATATGATCTCATCCATCCAAAGCAGAGGA 2678  
2208 TCCATCAATTTATGATTAATACCTGATGATCTATTAATAAAGAAACGAGGCGCA 2267  
2679 GGAATTCAGCTGAAGCCAGGGCACTTGAACCTCTCCGAAGAGATGTCTCAAGGTTTA 2738  
2268 GGGCATTCACCTTGAACAGAAAGCTTCAAGCTTGTGGAAGAGATCTTAAGGTATA 2327  
2739 TGAATGCAACAACTCCGCGCTTGTGTGGAGATTTTAAAGCATTTGAGATGAGG 2798  
2328 TGAATGAAAGACAGTTCTCTCAAGTCCATGAGGCACTTCACTAAATGAATCTTGGG 2387  
2799 GGTGACTTTGAACAGACATCCAGCAGTCTGTGGCTTGAATTTTCACTGATGCTGAAA 2858  
2388 GGTGATCTTAAACAGACATCCATCACTTGGCTGAGGATTCACACCAATGATCTGA 2447  
2859 CACACGAGAGGGCTTGAACCTGACCTTTCAGCTTGAACCTCAATCAATGATGAGAGCC 2918  
2448 CACCAACAGGTTTTCATCACTATACAGTTTGTATGATTAATGATGAGATTC 2507  
2919 AGGAACCCCAAGTTTGGCTAAGGTTATGATGAAGTCAATTTTGAAGGAGCTCCGT 2978  
2508 GGGCATCCCTAACTAAGGCTATATGATCCGTATGAAGGCCACTTAAACGACCTGATG 2567  
2979 GTCTTCACTGTGACCTTGATATCAGCTCTGGGGTATGAGAGACTGTGTGTGAG 3038  
2568 TCTGTACAGTTGCAACCGGGGTACCGCATGATGACACCAACCTTACCTGTTTGA 2627  
3039 TGGAGCGCCGAGACCTGGGACCGGCTCTGACCCTGTGTGCGCGAGGTGAGAGGAC 3098  
2628 TGAAGCAGAGAGTGTGGGAACCACTACTTGTGTATGACGAATGTGTGTGTA 2687  
3099 AGTGAAGAGAGGTGTCCGGGAGGTGTGATCAGCCGGGTATCCAGTCCCTATGAACA 3158  
2688 GATCCATGAGCAACATCAGAGCAATATTTGCTCCGTATCCAGCTCCGTATGACA 2747  
3159 CAATCTCACTGATCTGACCATGAGACAGAGCGGCTGTGACCATTTGGGCTTACATT 3218  
2748 CAACCTCCACTGACCTGATTAATGAGGACAGCCAGGAAGAACATTAAGCTTCATT 2807  
3219 CCTGTGTTGAACAGAGAGGTTCAGACGTCGCGCATCTGGGATGGGCTGTGA 3278  
2808 CATGTTTTCAGACCGGAATGGCTCAGACATCTCAAGTGTGGAAGGGCGGTGGA 2867  
3279 GAGCGGGTTCGTGTAAGAGAGTGAAGTGGCCCGGCTTGGCCAAAGACTGTGATGAC 3338  
2868 CAGTGAATCTCTGTGAAGAGTGAAGTGGCTCCGCTTCCGGAAGATCCAGACGAC 2927  
3339 CTTCAACTGAGTGTCTGAGTTCAGACTGACTTCTTCAACAGCAAGAGGCTTTTG 3398  
2928 CTTCAACTCACTACCTCAGTTCAGACGACACTTCTTCACTGAGAAAGTGTGGCTTTC 2987  
3399 CATTCATTTTCAAGTTCACAGCAACGTCCTGGAATGAACCTCGGGAATCCCGAAGATG 3458  
2988 CATCAAGTTCCTCACTCAATTTGACAGCACTGTATACAGATGATGCCCAATATGG 3047  
3459 GAGTGGAGTGTGACAGTTGGGAAGCCGAGCACTTCAAGTGTTCAGTGTGACCTTGA 3518  
3048 CACCCGCTATGAGAGACAGAGAGGCTGGAACACCGTCACTTCAATGTGACCTTGG 3107



3519 CTACGGCTGACGGGAAGTGCAGAGATCAGCTGTGTGAAGATCGAAGACAGGTTCTTCG 3578  
3108 CTATACGCTCCAGAGCAAGCCAAATATCACTGTGTGACGTGAATTAACCGGTTCTTTTG 3167  
3579 GCAGCCCAAGCCCGCAACATGATCGCTCCCTGCGGGGAGACCTGACAGAACATCTGG 3638  
3168 GCAACAGACCTCTCTACATGATAGCTGTTGTGAGGGAATCTGACGGGCCAGACAGG 3227  
3639 AGTATCTCTCAACCAATTAACCAAGCCCTAACCGGACGAGAGAGATGACTGAA 3698  
3228 TGTATTTTGTACCCCACTACCCAGCCGATCTCTGGAAGGAATGTGACTGAG 3287  
3699 AGTACCGCTCTACCAAGATTAAGTATCGCTGATGATTAATCATTTTAACCTGAGGC 3758  
3288 AGTAAAGGAACCCGGAATTTGTCTATCGCTGTGATTTTCAAAAGTTTAAATGAGGC 3347  
3759 TGGCTATGACTTCTTCATATCTAGACGAGGACTCTCTCAGCCCTCTCATAGAA 3818  
3348 CAGCTATGACTTCTTACATCATATGAAAGGGAAGTTCAACAGCCCTCATTTGGAG 3407  
3819 CTTTATGAGCTCCAGCTCCGAGCGGACTTGAAGCAGACCAACAGCTCTTCTGCG 3878  
3408 TTACAGAGGCTCTCAGGCCCCAGAAAGATGAGTACGGAACAGCTGTTCTGCG 3467  
3879 CTTCCGACGATGATCTGTGAGCAATGCTGAGCTTCTGATTTGATTAAGAAACCC 3938  
3468 ATTGAGATGATGCTCCGTGAGGCTTTCAAGGTTCCGATTTGAATTAAGAAAC 3527  
3939 GCGGAGTCAATTTTGTGATCTGTTCCATCAAGAACGCGACAGGGGTGCGACT 3998  
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3999 GAAAGTGGCTCTCCGCTACCTACTACTGACCAAGGGGCTACGAAGTTGAGGACCTC 4058  
3588 CAGGCTGAGTCAACCATCACTACAGTGAATCTGCTATPAAGATTTTGACCCCTC 3647  
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3648 ATTCATCACTGTGTGATTTGGGGCTGATGGAACCTCTGTGGACCAAGTCTGCTC 3707  
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3708 CTGCAATGCTCTGTGGAGGCGCAGTACAGGGATCAAGAGGGATGTTTTCACAA 3767  
4179 CTACCCCAAGACTACACAGTGAACAGATCGTTGATTTTGTATCTGTGCCAAG 4238  
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4068 ATGCAAGCTCTGTGCGGAGCCAGATACCGAAGAGAAATGTGTCTGAGTTTCTG 4127  
4539 GGCCTATGCTGCGCTTGAATGCAATCGGCTATGCTGCGAGGGGTGCGCAGAAATGA 4598  
4128 CTCATCTGCTCAATGAGTCAACCGGGAATCTGCTTCAAGGTTCAAGGCGCTCA 4187

4599 GTGCTCCCTGTGCTGGGAGCTTTGGCCCAATGAAATCTCAGGCGCCAGCTGTGTG 4658  
4188 CTGCAAGTCCGTGCCCAAGCCTTTGGCACATGGAACACAGATCCCAAGCTGTGTGT 4247  
4659 GCGGTGAGGCAACCTCACAGAGCGGAGCCATCTGTCTCCCTGCTTCCAGA 4718  
4248 ACCCTGAGTGCATTTCACTCAACGAAGAGTAACTCTGTCTCCCGCTTACCTGA 4307  
4719 GCGGTACTCAACAGCCCACTGTGTGTGAAGATGATGTGCTCCCGAAGGCGCTGAT 4778  
4308 GCGATACGAACCACTGAAGCTGTATGGAAGTCAATGTACGAGGGCTCGGAAT 4367  
4779 CCAGATCCAAAGTTGTCAAGTTTGTGACAGACAGACTGAGACTGCTGAAGTATTTGA 4838  
4368 TCAGATCAAGTATGATGATTTGCAAGAGACAGAACTCGGAACTCCTTGAGATCAAGA 4427  
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4428 TGTGGGAGTGTGACCGACCCAGACTGGGAAGCTTCTCAGGCAACAGATACCGGCACT 4487  
4899 TGTGAACGACCTTCCAAACGAGCTTCACTTCACTTCACTGATATCAGGATCTG 4958  
4488 GCTGAACGATCTTCAACCACTTACCTGATTTTCAAGTCTGATTAAGTGTGACAGC 4547  
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4548 TGCTGTGTTTCACTCGGAATACAAACCTGTAGTCTTGTGATGCAATGCAAGAACG 4607  
5019 GCCCATTAAGGGGTGAAGACTGCGAGCGCTACTTGGTGAATGATGTGTCTTTTCA 5078  
4608 CCCAGCAACAGCATCAAAATCGAGATCGGTATACGTGTGAACGACGCTCTCTTCA 4667  
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5028 CTTATTCACCTTTATATGATGACATTTGCAAAACCGGAAAGATTTAACTTGTAC 5087  
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5148 CTGGAATTAACGCGTGGGCAATCAGATCTTGTGAAGTATCTGTGATCAATTCAT 5207  
5619 TGGCAACCTGTCTCAAGTGTCAATGACCAACGGAATCGGACCAACCCCTGCTCC 5678  
5208 AGGCACTCTTCTCTCACTTGTACAGATGAGATCAACGAATCTGAACTACCTTTTCC 5267  
5679 CAAGTGTGAAGTCCCTGTGTGGGGAACATCACTTTCACAGGCACTGTGTACTCCC 5738



Db	5268	AAAGATGTGATGCCCCCTTTGGGTACAGGTAACTTTCTCAAGAGCGACCATCTACTCCCC	5327
Oy	5739	GGGGTTCCTTACCCCGTACTCCAGCTCCAGAGACTGTGTCGGCTGATCAACCGTCCCAT	5798
Db	5328	TGGCTTTCCTGTATGATATCCGATCCTGTAAAGACACTGATTTGGCTCATCAGGTGCTCCC	5387
Oy	5799	TGGCCATGGCGCTCCCGCTCAACTCAGCTGCTGCAAGACAGCCCTCTGAGATTTTCAT	5858
Db	5388	AGGGACCGAGATTTCATCTCACTTCACTCCCTGTTTACAGACGGAGCTGTCAACGATTTACAT	5447
Oy	5859	CACCATCTGGGATGGGGCCACAGCAACAGCAACAGCGCTCGGCTTACCACCGAGAT	5918
Db	5448	TGCTGTGGGACGGTCCCGATCAAACTCACCCGACGTGGGAGTTTTCAGTGTGCAACAC	5507
Oy	5919	GGCCCAAGAAACAGTGCAGAGATTCTCAACACGAGTCTGCTCAAGTTCCACCGTATGC	5978
Db	5508	AGCCTCGAAGACGGGTATAGTCCACCAACCAAGTCTTGCTCAAGTTCCACAGCACTT	5567
Oy	5979	AGCCACAGGGGGGATCTTGGCCATAGCTTTCTCGGCTTATCCACTCACCAATGCCCTCC	6038
Db	5568	TTCAATATGAGGCTTCTTTGTGCTCAATTTCCACGCAATTTCAAGCTCAGAATGTCAACC	5627
Oy	6039	TCCCAACCATCCCTCCCCAACGCCGAAGTGTCAAGAGATGAAGATTTCAATATAGTGA	6098
Db	5628	TCCCCACGCGTTTCCACAGGCAAGAAATCTTACTGAGGATATGATGTTTCGAGATAGGGA	5687
Oy	6099	CATCTGACGCTACAGATGCTCCCTGGGCTTAACTTATGAGGGGAAATGAATTTGACCTG	6158
Db	5688	TTTTGTGAAGTACAGATGCCACCCCGGTACACTTTGGTGGGACCGCACTTTGACTTG	5747
Oy	6159	CAAACTTGGAACTTACCTGCAGATTGGAAGAACACCCCGATATGTGAAGTGCACGTGCC	6218
Db	5748	CAAGCTCAGTTCCCGAGTTTGAGGGGTTCTCTCCCAACATGTGAAGCAATGCC	5807
Oy	6219	AACCAATGAGCTTCTGACAGACTCCACAGGGGTGATCTTGAGCCAGAGCTACCTTGAAG	6278
Db	5808	AGCAATATAGTCCCGAGCTGTGATCTACGGGAGTCACTTCAGTCCAGGGATTCGGGGTAA	5867
Oy	6279	CTATCCCGAGTTCCAGACCTGCTCTTGGCTGGTGAAGTGGAGGCCGCACTTAATCATCTC	6338
Db	5868	TTATTTTAACTCCCGACTGTGCTCTTGAGATTTAAATGTGAACCAACTCAACATTAAC	5927
Oy	6339	CCTCAGATGAGTACTTCTCAGCGAAGCAATATGATAGTTTGATTTTGATGG	6398
Db	5928	CATCTTGTGGACATTTTCAAAAGTGAABAGAGATTGATGACACTGGAAGTGTGATGG	5987
Oy	6399	TCATCAGGACAGAGTCTCTGTGTGAAGCCCTCAGTGGGAATTACTCAGTCCCCCTGAT	6458
Db	5988	TTCTTCTGGGCAAAAGTCCCTGTGCTGTAGTCTTAAATGGGATCACTAGTAAATCAATAA	6047
Oy	6459	TGTACCAAGCTCAAGCACTGTGTACTCTGGTGTGGTCACTGATACCGGTACATATCG	6518
Db	6048	TTTTCACAGCAGAGATTAATCAGTTATATCTCCGTGTGTCACGTACCTGACACAGTAA	6107
Oy	6519	GAAGGCTTCAAGATCCCGTATTTACGCCCTTACTGAGCTGTGCCAGGGCTCTCATCTCA	6578
Db	6108	GAAAGGATTTCAAGATTCGCTATGACGACCTTATCTGCAAGTTTGAACCAACCCCTGAAGAA	6167
Oy	6579	TGGCTTCAATCTAGGCCAGACAGCAACCAAGCCCGGGGGCTTCATCCACTTTGGCTCAA	6638
Db	6168	TGGGGGTATTTCTTAAACAGAGCTGACAGAGCGGTGGAAAGCAAAATGTCAATTTTTCGAA	6227
Oy	6639	CGCGGCGTACCGCCGTGTGGGACACAGAGATGGCCATCTGTACCCGGACACCCCGAGGCTA	6698
Db	6228	GCTTGATATCCGAATGTGTGGCCACAGCAATGCAACTGTGACGAAACCCACTTTGGCAT	6287
Oy	6699	CCACCTGTGAGCGAAGCCATCCCTCTGTCAAGCTTTTCTGTGGGCTTCTGTAGGC	6758
Db	6288	GTACCAGTGGGACTCCCTCACGCACTGTCCAGGCTGTGTCTGTGGAATCCAGAAATC	6347
Oy	6759	CCCCAAGATGGAATGTGTTTGGCAGAGAGTACAGTGGGAAACAAGGCCGTGTACG	6818

Db	6348	CCCAAGAAAACGGTTCATTATACCGGGAAACGAATTCACTTTGGACAGTAAAGTGGTCTATGA	6407
QY	6819	CTGCAGTGAAGGCTACCACTCCAGGCAAGCGCTAGAGCCACTGECAGATGTCGACAC	6878
Db	6408	ATGTCATAGAGGCTTTCAAGCTTTGATTCAGCCAGACAAACAGCCGGTGTGTAAGAAGA	6467
QY	6879	AGGCTTATGAGCAACCGCAATGTCACCAACAAGTGTGCTGTGTACTGTGCTGATGT	6938
Db	6468	TGGGCTGTGGAGTAAACAAGGGGAAGCGGCCCACTGTAAAGCCGGTCCCTTGCCCAACAT	6527
QY	6999	CAGTAAAGCATCAGCGTGAAGCAATGGCCGATAGGAGGCTTATCTTTGAGACACAGTATCGTT	6998
Db	6528	TGAAGCTCAGCTCTCAGAACATGTCATCTGAGGCTGCTGTTCCAGATCTTTGAATGAGTA	6587
QY	6999	CCAGGCCCAGCTGATGCTCATCTGTGACCCCTGCGTACTACTATCTGGCCAAAGGCTCAT	7058
Db	6588	CGGTGCTCAATATATTGCTGAGCTGCAGTCTCGGTACTTACTTAAAGCTGAGAGCTCT	6647
QY	7059	CCGCTGTACGCCCAATGGCAAAATGAGCCTCGGGAGCTTACGCCCACTTGCAGATCAT	7118
Db	6648	GCGGTGCCAGGCCCAATGGGACGTGGAAACATATGAGAGATGAGAGGCGCAAGCTGTGAGTTAT	6707
QY	7119	CTCCTGTGAGAGAGTCCCGAATTCGCCCCCAATGGCCACCGCATCGGAAACCTGTGTCTA	7178
Db	6708	CTCGTGTGGAAGCCTTTTCCTTTCCCCCAAAATGGCAACAGATTGGAAAGTTGACAGTTTA	6767
QY	7179	CGGGGCAACAGCCACTCTTCTCTCTCAATTCGCGATACACACTGGTGGGCTCCAGGGTGGC	7238
Db	6768	TGGGGCCACAGCTATATTATACGTGCAACACCGGCTTACAGCTTGTGGGGTCTCATGTACAG	6827
QY	7239	TGAATGCATGGCCAAATGGGCTCTGGAATGGCTTGAAGTCCGCTGCTTCTGTGACACTG	7298
Db	6828	AGAGTGGCTTGGCAATGGGCTCTGGACGGGACGGAACATCGATGTCTGGCTGGCCACTG	6887
QY	7299	TGGGATCTCTGAGGCCATTTGTCAACGACACATATAATGGGGAAGACTTACAGCTACCGGGG	7358
Db	6888	CGGTTTCCCAACCCGAGTGTGAAACGGTGTCAATTAAATGGAGATGGCTTACAGTTTACAGAGA	6947
QY	7359	CAGTGTGGTGTACCAATGCAATGTGTGGCTTCCGCTCATCGGCAATGTCGTGGCCATCTG	7418
Db	6948	CAGGTGTGTTTACAGTGTCAATCTGTGGTTTCGGGCTTGTGGGAATCTTCGTGAGGATATG	7007
QY	7419	CCAGCAGGATCATCACTGTGTGGGCAAGACCCCTTCTGTGTGCAATTAACCTGTGACACA	7478
Db	7008	CTCTCAAGAACCAAGTGTGTGGAACAAACGCGTGTGTGTGCCATCAACATGTGTCA	7067
QY	7479	CCCAAGGCAACCTCTGTCAACGGGCTCACTCAGGGTAAACCAATTTAACCTCAACGATGTGT	7538
Db	7068	CCCTGTGAAACCTCTGCCACGGAATTCATTAATGGCAGTGAAGTTCAACCTGATGATGTGCT	7127
QY	7539	CAAGTTTGTTTGCAACCTGGGTATATGGCTGAAGGGGGCTGTAGTGTCCCAATGGCCGGC	7598
Db	7128	GAAATTTCACTGTCAACACGGGCTATTGTTGTGCAAGGGGGGTGTCTGAGCCCAAGTGTGGAG	7187
QY	7599	CAGCGGGCAATGAGTGTACATGTCTGCCACCTGCAGATCATCAACTGTACAGATCTGTG	7658
Db	7188	CAAGGGCCAGTGGAGTATGCTCTGTGCCCAAGTGTCAAGTGTGAACGTGTTCTGATCCAGG	7247
QY	7659	ACACCAAGAAATATGTGTGTGTGTCAGTTCACGCCAGCGGCGCCGACAGTTTCAAGCTTCCG	7718
Db	7248	CTTTGTGGAAAAATGCCATTGTGTCACGGGCAACAGAACTTCCCTGAGAGTTTGAATGATGG	7307
QY	7719	CACACATGTGTCTTAACGGGTGCAACACAGGCTTCTACTCTGTGGCAACCCCAAGTGTCAAG	7778
Db	7308	AATGATGATCTGTACATTTGCAAGAAAGGAAATTTTAACTTGTCTGGGATCTTCAACCTTGAC	7267
QY	7779	CTGCCAGGAGATGGACATGGACCGTCCCGGCCCAAGTGTCTCTGTGTCCTGTG	7838
Db	7368	CTGTATGGCAAAATGCTTATGGGACCGATCCCTGTGCCCAAGTGTGTTGGCTATATTCGTGTG	7427
QY	7839	CCATCCGGGCTCCCGGCTCACTTCCAGATGTCTGAGACAGTTATATCTGTGGAGCAGT	7898
Db	7428	ACACCCCAAGGGGTCCCTGTCCCAACGCGCTTCACTGTGGAGACCTGTATTAACATATGGCGCGT	7487

QY	7899	GGTGGCGGTAAAGCTGCTATGCGGCAAGCGTAATCTGTGTGGGAAAACAGGACCCGAGTGTGTG	7958
Db	7488	CGTGCACTACTCTCTGCAGAGAGAGCCGAGACCTCTATAGGCACAGACACGAGTGTGCCA	7547
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Shinkler, R.A., Lichenstein, H., Vernet, C. and Fernandez, B.  
 TITLE Polypeptides and nucleic acids encoding same  
 JOURNAL Patent: WO 0136638-A 31 25-MAY-2001;  
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 REFERENCE 1  
 Shinketsu, R.A., Lichenstein, H., Vernet, C. and Fernandes, F.  
 Polypeptides and nucleic acids encoding same  
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 A novel giant gene CSMD3 encoding a protein with CUB and sushi multiple domains: a candidate gene for benign adult familial myoclonic epilepsy on human chromosome 8q23.3-q24.1  
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 MEDLINE  
 PUBMED  
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 Db 2808 GAATTTGATGTGGTATTTGAAGCTGAACCTGGAACCTGTATCAAAATTAATTTGAAG 2867  
 Qy 1665 ATTCAAAACGAGGTCACTATGAACCTGTGAAGTACGGATGGCGGACTTACTCAGC 1724  
 Db 2868 ATTTCAGACTGAATGATATGATTTCTGGAAGTTCAATGAAGGCCCAAAATCTTCTGTC 2927  
 Qy 1725 GCGCTGATGGGGTTTACAGAGGAGCCAGGTTCCCAAGTTCTCATCAGACAGCA 1784  
 Db 2928 ACCCTGTGTGATCTTACATGACACCAAGTCCCAAGTTCTTATTAATGAGCTGA 2987  
 Qy 1785 CTACTCTACCTCTCTCTCTCAACGACAGAGCTCACTGGACATGCGCTTCAGCTCCG 1844  
 Db 2988 TTTTATATACCTTCTATTAACAAGCAACAGTCTGTCATTAATGATTAAGATTA 3047  
 Qy 1845 CTATGACATTAACACTGACATGACCACTGTCTGATTCAGGAATCCCACTAATG 1904  
 Db 3048 TTATGAAGTGTAAAGTGAACGTAATTTCTTTGTAACCTCTGGCATACCTGTATATG 3107  
 Qy 1905 ACAGCGCATGGGATGATCTTCAAGTGGGCGCTGTGACCTTCAAGCTGTGATCGG 1964  
 Db 3108 CCGTGTATGTGATATATTTCTCACTGCTCACTGTTTCAATTAATGATTAATGAG 3167  
 Qy 1965 CTACACATTAAGTACGGGAGCTCTGAGTGTGAGCCCACTTCAAGTGAAGCGGCG 2024

Db 3168 ATACAGGTGATGATGAAGGCCCTTATATGCAAAAAAACCACTGTGTGATCATCC 3227  
 Qy 2025 CTGCGCAATTTGTAAGCTCTGTGTGCTTCAATTAAGGCTCCAGTGGACCACTT 2084  
 Db 3228 ACTTCCAACTGTGATGATTAATGAGGAGATGTTAGGGGCTGATGGAACCACTT 3287  
 Qy 2085 GTGGCAGGGTCCCTGATCTTACCCCAACTTGAACCTGACCTGATTAATGAAAC 2144  
 Db 3288 ATCACTGTGTTACCCGGAATTTTATCAAAATCTGTGAATTTGATCAATGATGATGT 3347  
 Qy 2145 ATCTCATGCAAGGTTGTCTTCACTTTCACACCTTCACCTGGAAGTGGCCATGA 2204  
 Db 3348 AACCATGAAAAGGTGTGACGTTCAACTTCCACACTTTTCAATTTGGAACCAATCATGA 3407  
 Qy 2205 CTACTCTCTATCATGTAAGACGACCTTACCCAGCCCTGAGGAGTAACTGTATC 2264  
 Db 3408 CTACTCTGTATCAAGAAATGGAATTTTACCAACCACTGACAGCTGATGATGTC 3467  
 Qy 2265 TCGGCTGCAAGCTCCCATCAGCGCTCTATGCACTTCCAGCTCCAGGTCGCTT 2324  
 Db 3468 AGATCTTCTCCAAACATCAATGATGCTGTCTATGGAATTTTCAAGGCTCAATTTGCGTT 3527  
 Qy 2325 CATCTGATTTCTCATGATTAATGAAGATTTCACTACCTTCTGAGATGCACTT 2384  
 Db 3528 CATTCAGATTTTCAATATCAATGAAGATTTTAAATTAATTAATTAATTAATTA 3587  
 Qy 2385 GGAACCTGTGAGAGAGCCGAGCTCCAGCTCAAGATCGGAAGGCTTGCAGTTGG 2444  
 Db 3588 TGAACCTGTGAAATATCTGCAATCTCAATATGATGATGATGATGATGATGATGAT 3647  
 Qy 2445 CGTGGGCAACCTTGAACCTTCTCTCTTCCCGGATCCGCTGAGAGGACCGCCG 2504  
 Db 3648 GATTTGATGACCTGACCTTCTCATGCTCTGTGGGTTATGATGAGAAAGAACATAGA 3707  
 Qy 2505 CATACGCTCTGGGGGAGACGCGCTGTGAGCTCGCTTCTGCAAGTGTGTC 2564  
 Db 3708 GATCATCTGTCTGTGTGTGCGGACGACAGTGTGAGACCTTGTGCAAGTGTGTC 3767  
 Qy 2565 TGAGTGTGGAAATTCAGTCAAGGACCTCAGGTAATTTGCTGCTCCCACTTCTCTGT 2624  
 Db 3768 TGAATGTGTGATCTGACAGAAATTAATGAAGAAATTTGCTGCTCCAAATTTATCACT 3827  
 Qy 2625 GAACTATTAACATATGATGATGATCTTCCATCAAGCCAGCCAGGAAAGGAAT 2684  
 Db 3828 CAATATTAACAAACATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3887  
 Qy 2685 TTAGTGAAGCCGAGGATTTGAACTCTCGAAGAGATGCTCTCAAGTTTATGATG 2744  
 Db 3888 CAATATTTCAAGCAACATTTCAATTTAGCAAGAGAGATGCTTAAATTAATGATG 3947  
 Qy 2745 CAACAAACCTCCGCGCTTGTGAGGAGTTTATGACATTTCTGAGATGATGAGGAGTAC 2804  
 Db 3948 AAAAGATTAACGACTATCTACTAGTGTCTTTTATGATGATGATGATGATGATGAT 4007  
 Qy 2805 TTTGAACGACATTCAGACGCTGTGTGATTTATCACTGATGATGATGATGATGAT 2864  
 Db 4008 ACTTGTGTGATCTTCAATCACTGTGTGATTTAATTTCCATCTGATGATGATGATGAT 4067  
 Qy 2865 CAAGGCTTTGAATGACCTTTTCAAGTTGAATCACTCAAAATGATGAGGCCAGAGAC 2924  
 Db 4068 TGAAGCTTTCAACTGTGTATACCAAGTTTGAATCTCAACATGATGAGATCTCGGAT 4127  
 Qy 2925 CCCCAAGTTGGCTCAAGATTTCAAGATGATGATGATGATGATGATGATGATGATGAT 2984  
 Db 4128 TCCACAAATTTGATTAAGATCAAGTACCAAGGACCTTGTGTGATGATGATGATGAT 4187  
 Qy 2985 CAGCTGTACCTGTGATCAAGCTGTGAGGATGATGAGAGCTGTGTGTGATGATGAT 3044  
 Db 4188 TGAATGATATCAAGCTTCACTCCAGGAAGTACCTTCTCAAGTGTGATGATGATGAT 4247  
 Qy 3045 GCGCGGACCTGTGAGCGGCTTGTGCACTGTGTGCTGAGTGTGAGGAGGACAGTGA 3104  
 Db 4248 GAGAGGAGCATGAGCTATCTGTGCTTCTGTATGCTGAATGATGAGGATCTTTTAA 4307

OY	3105	AGGAGAGGTGTGGGGCAGGTGCTGTACACCCGGGATTCACACTCCATAGAACACANTCT	3164
Db	4308	AGGAGAAATCAATCAGAGAAATCTTATCTCCGGCTATCTCTTTCCATATGCAATTAACCT	4367
OY	3165	CAACTGCATCTGSCACCATCGAAGCAGAGGGCCGGCTGCACCATTTGGGCTACACTCTTGAT	3224
Db	4368	GGCTTGCATGTGTGATGATTTGAGATGATCCTCGGAATTAATTGTACGCTTGCACTTTCTTGC	4427
OY	3225	GTTTGACACAGAGAGGTTCAAGACGTGCTGCGATCTGGAGTGGGCTGTGAGACGG	3284
Db	4428	TTTGTATTCGGAAGACATCAATGATATTACTCCGAGTCTGGACGGTCCACCAAGAAATGA	4487
OY	3285	GGTTCGTGTGAAGAGCTGAGTGGCCGGCCCTGCCAAGACCTGCATAGACCTTTCAA	3344
Db	4488	TATGCTTTTAAAGGAATTAAGTATGATCTCTTATATCTCGAAGAAATTAACATAGCACTCCAA	4547
OY	3345	CTGGGTGCTCTGCGAGTTCCAGACACTGATCTTCTTCCACGACAGAGAGGGCTTTGCATTTCA	3404
Db	4548	TATAGTAAACATCCAGTTTGACAGGATTTTATTAATTAGCAAACTGTGATTTGCAAATTTCA	4607
OY	3405	ATTTTCAGTGTCCAAGCAACGCTCCTCGAATAGACCTTGGGATTCGCCGAGATGGAGATCG	3464
Db	4608	GTTTTCAAGTCTGTGTGACACTGGGTGTGTGACCCAGGGTCCCAATGATATGGGACTCG	4667
OY	3465	GAGTGTGACAGTTGGGAGCCGGCGACTCCACAGTGTTCAGATGTGACCTGTGCTACGC	3524
Db	4668	AAATGGGATGTGAAGAGAACTGGGGGACACTGTTGTTTTCAAATGTGACCCAGAGTATATGA	4727
OY	3525	GCTCGAGGGAAGTGCAGAGATCAGCTGTGTGTAAATCGAAGAACAGTTCTTTCTGGCAGCC	3584
Db	4728	ACTTCAGAGGAGAGGAAGAAATTAACCTGTGATTCAGGTAAAGAAATCGGTACTTGTGGCAGCC	4787
OY	3585	CAGCCCGGCAACATGCATCGCTCCCTCGGGGGGAGACTGACAGAGACCATCTGAGATCAT	3644
Db	4788	CAGCCCAACAGCTGTATATAGACACCTGTGTGAGGCAATTTAACAGATCTTGAGCTTTAT	4847
OY	3645	CCTCTACCAAAATTAACCGAAGACCTTACCGGCAAGGCAAGAGTGTGACTGGAAAGTGAC	3704
Db	4848	TCTTTCAACAACTTCCCTCATCCATATCCGCAATAGCAGAGACTGTGACTGACTATAC	4907
OY	3705	CGTCTACCAACATACGTCATCGCCCTGTGTATTTAACATCTTTTAACCTGGAGCTTGCTA	3764
Db	4908	CGTCAATGCAACATATGTTATCTCTTGGCGTTATCACTTTAGCAATGAAACCAACTA	4967
OY	3765	TGACTTCTCCAAATCTACGACGAGCGGGACTCTCTGAGCCCTGCATAGGAACCTTCTA	3824
Db	4968	TGACTTCTCTTATATCTATATGATGAGCCAGACAGTATATGCCACTGATGTGAAATTTTCA	5027
OY	3825	TGGTCTCCAGCTCCAGGCGGCACTTTGAAAGCAGACGAACGCTCTTCTCGGCTTCCG	3884
Db	5028	AGACAGCAAGTTTACCAGAGAGAAATGAAAGCAGCTCAAAATACATGCACTTTGGCTTTTCG	5087
OY	3885	CAGCGATGCATCTGTAGCAATGCTGCTTGCTCATTAATACATACAGAAAACCCGCGGA	3944
Db	5088	GAGTATGATGATCTGTTAGTTTACACTGGAATTTCACTGAAATTAACAAAGCAAAACTGCGAGA	5147
OY	3945	GTCATGTTTTTATCCTGTGTTCCATCAABAAGGCAACGSGGTGGGTCGCACTGAAGCT	4004
Db	5148	GTCCTGCTTTATCCAGGCAATATATATAAATGGCCAGACTTGGAATGATATTAATTT	5207
OY	4005	GGGCTCTCCGTCACCTACTACTGCGACGGGGGCTACCAAGTTGAGGGCACTCGACCT	4064
Db	5208	AGGCTCAACAGTCACTTATCTTACTGTGATGCTGTGTTATGTTCTTCAAGTTATTTCAACCT	5267
OY	4065	GAGCTGCATCTTGGGGCTGATGGGAAGCCGTGTGAACAATCCCGGCCAGTCTGCAC	4124
Db	5268	CACCTGTATCATGGGAGATGATGGAAGACTGATGAAATGAGGCTTGCCAAAGTTGCA	5327
OY	4125	AGCCCCCTGTGGGGACAGTATGTGGGTTTCGAGCGAGATGGTCTTTGTCCCAACTACCT	4184
Db	5328	TGCGCCCTGTGGAATCGTTCAACAGGTTCAAGAAAGCACTGTCTCATCAACCAACTATCC	5387

QY	4185	CCAGAACATACACAGTGGACAGATCGTGTATATTTGTTATCTGAGGCCAAGGACTATG	4244
Db	5388	AAAAATTAACGTGTGGACATAATGTGTTATTTCTATAGCAAGTTCCAAAGCACTTGT	5447
QY	4245	GGTGTGTTGGCCAGATTCGCTCTTCTTCAACGCGCCTCAACAGACGTGTGAGGTTTCA	4304
Db	5448	GGTGTGTTGGCCAGTTTGTATTTTTCACAGATCACTCCAGATGTGTGTGAGGTATGA	5507
QY	4305	CGGCGACAGCAGCACTCGCGGCTCTCAGCTCCCTCTCGGGCTCCATACAGAGAAATC	4366
Db	5508	TGGGCGCACTCAGCAATCTTCTGTGTATCTTCCCTCCAGAGATCCCATTCAGAGAAATC	5567
QY	4365	ACTGCCCTTGGCCACCTCCATCAAGTCTCATTAAGTTCAGCGCCAAAGGCTCGCAC	4424
Db	5568	ACTTCCACTGAGTTAGGTATACAGATCACAATTCGATTACTTCAAGTTGACCAATTAAC	5627
QY	4425	AGCCAGAGGCTTCCACTTGTGTCTAACAGCGGTTCTTCGAACACAGCCCAACGACAGTGCAG	4484
Db	5628	AGCTAAGGGAATTTCACTTTTGTATACAAAGCTGTTCCTAGAACAAAGTTCTACACAATGAG	5687
QY	4485	CTGTGTGCGGAACCCCGCTATGCGCAAGGCTGGGCGATGACTTCTCGGTGGGGCCAT	4544
Db	5688	TTCTGTGCTGAACCAAGATTCGGAGAAAGAAATTTGCACATGAATTTGGACGTGGTTCAATC	5747
QY	4545	CGTCCGCTTCAATGCAACTCCGCGTATAGCCCTGACAGGGGTGCGCAGAGATCGAGTGCCT	4606
Db	5748	GGTCTTTTATTTGTATATCCAGAGATATATTTCTCCATGATTCATAGCAATTAAGTTGGA	5807
QY	4605	CCGTGTGCTGGGGGCTTGGCCCAATGGAATGTCTACCGCCCAAGCTGTGTGGTGCCTG	4666
Db	5808	AACAGTGCCTCAATTTCTTTGGCCAGTGGAAATGATTTCTTACTCTATGTATATGTGCCCTG	5866
QY	4665	TGAGGCAACCTCACAGACGCGAGGGGACCATCCTGTCCCTGGGCTTCCAGAACCGTA	4724
Db	5868	TGTGTGAATTTTAATACTAAGCCAAAGGACATATTTGTCACTGGATACCCCGAGCTTA	5927
QY	4725	CCTCAACAGCTCAACTGTGTGTGGAAGATGTGTGTCCCCGAAGCGCTGGCATTCAGAT	4788
Db	5928	TGACAAACATCTGAATGTGTGTGGAAGATCAAGTGCAGAGGAGCTGTGCATTTCAAGT	5987
QY	4785	CCAAGTGTCAAGTTTGTGACAGACAGAACTGGGAACTCGCTGGAAAGTATTTGATGTGAC	4844
Db	5988	GCAGTTTATAGCTTTGTCTACAGAACATTAATGGGATTTCTTGACCTTTTAATGATGGGG	6047
QY	4845	AGATTAACCTGTAAACCATGTGTGGGAGTTTCTCAGGAACAACCGTGCCTGCCCTTCTGAA	4904
Db	6048	AGACAAACATGCTCCAAAGACTTGGAAAGTATTCAGGAACAACATPACCCACTTTTGA	6107
QY	4905	CAGACCTTCCAAACGACTCTAATTTCTACTCAGATATCAGCGTATTCGACGTG	4966
Db	6108	TAGTACGCTAATTAATCTGTATCTTAATTTCAATCAGACATCAGTGTTTCTGCTGCAGG	6167
QY	4965	CTTCCACTTGGAGTACAAACGATGGGCTGACAGATGTCGCGAACCCTGCTGTGCCAG	5024
Db	6168	ATTTCATCTTAATAACAGACAATTTGGTTGTGATTCCTGTCTGAACCAAACTCTCAG	6227
QY	5025	TAAACGGGTGAAGACTGGCGAGCGCTACTTGGTGAATGATGTGTGTTTCCAGTGTGA	5084
Db	6228	CAGTGAATTTAAATTTGGAGACAGATATATGTGTGAGATTTAGTATCTTTCACTGTGA	6287
QY	5085	GCCGGGATATGCCCTCCAGGGCCAGCCCAATCTCTGATGCCCCGGAACAGTGGCGCG	5144
Db	6288	TCAAGGATATTTCTTTCAAGGGTCACTGCATTAACATGATGACGAGGACCTGTAAAG	6347
QY	5145	ATGGAACATCACTCTCTCACTCTGTATTTGACAGTGTGGGGGAACAGTGAAGAGATGGA	5204
Db	6348	ATGGAATTAATCCAATCCCAATTTGTTTATGCTAGTGTGTGTGTCTATGTCAAGCTTACG	6407
QY	5205	GGGGGTGAATCTGAGACCCCGGCTTCCAGGGGAATCAACCCAGTAACATGACTGCTCTG	5266
Db	6408	TGTGTATATCTCACTGCTCTGGGTTTCTGTGAATCATATCCAGCAGTTTAATGTGCATGT	6466
QY	5265	GAATAATGACATGCCCGTGGGCTTTTGAGACTCAATCCAGTTTCTTCAACCGA	5324

Db 6468 GACAAATAATCTAACCAATAGGTTTGTGTATCATCTCCAGTTTGTAAATTTTCTACAGA 6527  
 Qy 5325 GCCCAACCAAGCACTACATAGAAATCCGGAAATGGCCCTTATGAGACCAGCCGATATGG 5384  
 Db 6528 AACCAATACATGATTTATTTGGAGTACGAAGTGTATCTCAGAACTAGTATGTATGG 6587  
 Qy 5385 AAGATTACGTGGAAGGAGCTTCCAAAGCTCCCTCTCTCAGTCCAGCCAGACCAAGCT 5444  
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 Qy 5505 TGAATCTTGAAGAGTGGCCAGACCCAGAGCCCTTGGCAATGGCAATTTGAGGGAGCTGG 5564  
 Db 6708 TCAAGTTGCAAAAGCTGCTGATCCAGCCGTTTGGAAATGGTTTGTAAATGGTAAATGA 6767  
 Qy 5565 CTACAAAGTGGAGCAATCAGTACCTTGAGTGGCTCCCGGGGTATCAATGACTGGCCA 5624  
 Db 6768 TTTTACTGAGGTCAAAACATTTTCAATTTGAATGTTTCCAGATACACATTAATTTGAAA 6827  
 Qy 5625 CCTGTCTCAGCTGTCAACATGGCAACCAACGGAATGGGAACAACCCCTGGCCAAAGTG 5684  
 Db 6828 TTCAAGTCTCAGATGCTTCAAGAGTCACTGTATTTGAATTCATCCACTTCCAAGGTG 6887  
 Qy 5685 TGAAGTCCCTTTGGCGGGGAATCACTCTTCCAAAGCACTGTGTACTCCCGGGGT 5744  
 Db 6888 TGAAGCTCTTTGTGGGGAATTAATGCAATGAATGGCACATTTATTTCTCTGGGTA 6947  
 Qy 5745 CCTAAGCCGTACTCAGCTCCAGAGCTGTGTGGCTGATCACCGTCCCATTTGGCCA 5804  
 Db 6948 TCTGTATGATATCCAAATTTTCAAGATTTTGTGGCTTGTAAAGTATCCCTGGGA 7007  
 Qy 5805 TGGCGTCCGCTCAACCTCAGCTGTGTGACAAGAGCCCTGTGAGATTTGATCAACAT 5864  
 Db 7008 TGGCATCTACATCAATTTTACTGTCTTCAACAGAACAAATATATGATTTCAATAGCT 7067  
 Qy 5865 CTGGATGGGCAACAGCAACAGCAACAGGCTCGGCGCTTCAACCCGAGATGGCCA 5924  
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 Qy 6165 TGAACCTACCTGAGTTGAAGAACACCCCGATATGATGAGTGCATGTCCAAACA 6224  
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 Qy 6225 TGAAGCTTGAAGACTCCAGAGGCTGATCTGAGCCAGAGACTACCTGGAAGTATCC 6284  
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 Qy 6285 CCAAGTTCCAGACTGCTGTGGCTGGTGAAGTGAAGCCGACTATTAACATCTCCCTGAC 6344  
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 Qy 6345 AATGAGTATCTTCTCAGGAGAAAGCAATATGATGATTTGATGATGCTCATC 6404

Db 7548 TGTAAATTTCTTCCAGACAGAAAAAGAAATTTGATGTTCTTCAAGTGTATGATGACCAAA 7607  
 Qy 6405 AGGACAGGTCTCTGCTGGAAGCCCTCAGTGGGAATTAACAGCTCCCTGATGTGAC 6464  
 Db 7608 TATTTAAAGTCAAGCTTATTTTCCCTCAGTGGGATATTTATCATCTGCTTTTAAATATAC 7667  
 Qy 6465 CAGCTCAAGAACTCTGTATCTGCTGTGTGATCATGATCAAGCTTCAATTCGAAAGG 6524  
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 Qy 6525 CTTCAGATCCGCTATTCAGCCCTTACTGACGCTGCCAGGGCTCCATCTCATGCTT 6584  
 Db 7728 CTTCGGAATGAATATATAGCTTTTCTACTGTAGTACACAGAAATCCCACTCATAGATA 7787  
 Qy 6585 CATCTAGCCAGACCAAGCCAGCCCGGGGCTCCATTCACATTTGGCTGCAAGCCGG 6644  
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 Qy 6705 GTGAGCGAAGCATCTCTCTGTCAAAGCTTTTCTGTGGGCTTCTGAGCCCA 6764  
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 Db 7968 AAATGAGAAATCTACACACAGACTATTTGTATGAAAGCGAGTTACTTATTTTGTAA 8027  
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 Db 8208 CAAAGTATTTTACAGCTGTGACCTGGTATCAAGATATAGTCTGCTCATGAGATG 8267  
 Qy 7065 TCAGCCAAATGCAATGAGACCTCGGGACTTAAGCCCACTGCGCAATCATCTCTG 7124  
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 Qy 7125 TGGAGAGCTCCGGAATCCCGCAATGGCAACGCAATGGGAACATGCTGTATAGGGGC 7184  
 Db 8328 TGGAACTACTACACTCTCAAAATGGAATTAAGATTTGAATCTAACTTCAATATGCTC 8387  
 Qy 7185 AACAGCAATCTTCTCTGCAATTCGGAATCAACACTGTGTGGCTTCCAGAGTGTGAGTG 7244  
 Db 8388 AAACGCTATCTTTACCTGCACTTGGATCATGCTTGTGGCTGTGATAGGGAATG 8447  
 Qy 7245 CATGGCAATGGGCTCTGAGTGTCTGAAAGTCCGCTGCTTGTGTGACACTGTGGAC 7304  
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 Qy 7425 GGATATCATCTGTGGGCAAGACCCCTTTTGTGTGCAATTAACCTGTGACACCCAGG 7484  
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QY 7485 CAACCTGTCAACGGCTCAGGCTAACAGTTTAACTCAAGATGTGTCAAGTT 7544  
 DB 8688 TAGTCAATTTTATGAAAGAACAGTGAATGGGTTCACTTTAAAGATGTGTAACTTT 8747  
 QY 7545 TGTGTGCAACCTGTGGTATATGCTGAGGGGCTGTAGTCCCAATGGCTGGCCAGCG 7604  
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 QY 7605 GCAATGAGTGAATGCTGTGCTCCCACTGCAAGATCATCACTGTACAGATCTGGACACA 7664  
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 DB 8868 AGCAATTTCTTAAAGAAAGTAA--ATAGAACTGGAAATTTTACTTACGGCACTGT 8924  
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 DB 8925 GGTATTTCTATGACTGCAATCTGTGATATTTTATTTGATCTTCAAGTTTGTATGTCA 8984  
 QY 7785 GGGAGATGGCACTGGGACCGTCCCGCCCACTGTCTTGTGTCTGTGTGCAATCC 7844  
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 QY 7905 GTACAGCTGATCGGCAAGGCTACTGTGTGGGAAACAGCAACCGCATGTGTGGCTGCA 7964  
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 QY 7965 TGGACACTGAGCTGCTCCCTCCTCACTGTGTGAGAACAGGCTGGAGTTTGGGTGA 8024  
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 DB 9225 TCCAGGTACTCCCGGCTATGGCTGTAGACAGAAACATTTTGAATCTTAAAGTACTGT 9284  
 QY 8085 GCGCTTCAAGCTGTGAAGCTGGCAGCTGTCTCCGGGATCGTCAAGGCGCACTGTCAAC 8144  
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 DB 9405 AACCAAGCCAAATGGAAGGTTCTTCGAATTTGATGCAACAATTTTCTTATGCTCACT 9464  
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 QY 8445 GTGTGTCCCTGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8504  
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 REFERENCE 1  
 AUTHORS Shimizu, A., Aakawa, S., Sasaki, T., Yamazaki, S., Yamagata, H.,  
 Kudoh, J., Minoshima, S., Kondo, T. and Shimizu, N.  
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 Biochem. Biophys. Res. Commun. 309 (1), 143-154 (2003)  
 JOURNAL 12943675  
 MEDLINE 2824680  
 PUBMED 12943675  
 REFERENCE 2 (bases 1 to 13148)  
 AUTHORS Shimizu, N., Aakawa, S. and Shimizu, A.  
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 160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp,  
 Tel:81-3-3351-2370, Fax:81-3-3351-2370)  
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QY 3525 GCTGCAGGAGATGACAGATTCAGCTGTGTGAAGATCGAGAACAGGTTCTTTGGCAGCC 3584  
DB 4836 ACTTCAAGAGAGAGAAAGAAATTAACCTGCATTCAGGTAGAGAAATCGGTACTTTCGAGCC 4895  
QY 3585 CAGCCGCGCAACATGATGCTGCTCCGCGGGGAGACCTGACAGGACCATCTGAGTCAAT 3644  
DB 4896 CAGCCACAGCTGTATGACACCTGTGAGAGCAATTTAAAGAGATCTTCAGGCTTTAT 4955  
QY 3645 CTTCTACCAAAATTAACCAAGACCTTACCCGAGGCAAGAGTGTGATCTGAAAGTAC 3704  
DB 4956 TCTTTACCAAACTTCCCTCATCATATCCGATAGCAGAGACTGTGACTATCAC 5015  
QY 3705 CGTTCACAGACTAGCTCATTCGCCCTGTATTTACATCTTTTAACCTGAGCTGCTA 3764  
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QY 3765 TGAATTCCTCATATCTAGACAGGACGGAAGCTCTCAGCCCTCTCATAGAAAGCTTCTA 3824  
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QY	6825	TGAAGGCTAACCACTCCGAGGAGCGCTGAGAGGCCACTGACAGATGTTGACACAGGCT	6884
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QY	6885	ATGAGCAACCGCAATGTCCACCACAAGTGTGCTGTGTGACTTGTCTGATGTCAATAG	6944
Db	8196	ATGAGCAATCATTAACAAGACCCCTCGCTGTGTGTGTGTATCATGTCCAAAGCATCAATTC	8255
QY	6945	CATCAGCTGAGAGATGGCCGATGAGAGCTTATCTTTGAGACACAGATATCAGTTCCAGGC	7004
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Db	8376	TCTTCTTAATGGTACTTGGAGTGGAGAAATGAAAGAACATATTGCCAAATTAATTCCTG	8435
QY	7125	TGAGAGCTCCCGATTTCCCCCAATGGCCACCGCATGGGAACATGTCTGTCTACGGGC	7184
Db	8436	TGGAAATCTACTCACTCACTCCAAATGGAAATGAATTTGGAATCTAAATTCATATGGCTC	8495
QY	7185	AACAGCCATCTTCTCTGCAATTCGCGATACACTGGTGGGCTCCAGGGGTGCTGATGT	7244
Db	8496	AACAGCTATCTTTACTCTGCACTTGGGAATTAATGCTTGTGGGCTCTGTGTGAAGGAATG	8555
QY	7245	CATGGCCAAATGGGCTCTGAGTGGCTGGAAGTCGCTGCTGCTCTGTGACACTGTGGAC	7304
Db	8556	CCTTTCTCAAGTCTTTGGAATGGAATCGAAACAGATGCTTAAGGGTCAATTGTGAAAT	8615
QY	7305	TCCTGAGCCCATTTGTCAACGACACATTAATGGGGAACCTACAGCTACCGGGCACTGT	7364
Db	8616	TCCAAACTGATTTGGAAATGGTCAAGTATTGGAAATTAATGATATAGACACAGT	8675
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Db	8796	TAGTCCAAATTAATGMAAACAAGTGAATGGGTTCAACTTATATGATGTGTGAACATT	8855
QY	7545	TGTTTGCAACCTGGGTATATAGCGTGAAGGGGGCTGTAGGTCCCAATGCCGGCAGCGG	7604
Db	8856	CTCATGCAATATTTGGGTATCTTATGCAAGGGCAACAAAGGACAGTGTCCAGGCCAAG	8915
QY	7605	GCAATGAGTGCATGCTGCCCACTGTGAGATCATCACTGTACAGATCTCTGACACA	7664
Db	8916	ACAGTGGAGCCATCTCTCCACGATGTGAAGAAAGTGTCAACTGTGTGATCTCGAATTC	8975
QY	7665	AGAAATATGTGTTGCTCAAGTTCACGCAAGCGGGCCGCAAGGTTCAAGTTGGCACAC	7724
Db	8976	AGCCCAATTTCAAAAGAAAGTAATA--ATAGAACATGAAATTTTACTTACGGCACATGT	9032
QY	7725	TGTGTCTTAACGGTGCACAACAAGGTTTCTAAGTCTCTGGGCAACCCAGTGTCAAGTGA	7784
Db	9033	GGATATCTATGACTCAATCTCGAATATTTTATTTATGATCTTCAAGTTTGAATATGCA	9092
QY	7785	GGGAATGAGCATGAGGACCGTCCCCCGCCCAAGTGTCTTTGGTGTCTGTGGCCATTC	7844
Db	9093	ACCAATATGACATATGGACAAACCTTTACAGAAATGATATCATGATGACTGTGGACACC	9152
QY	7845	GGGCTCCCCGCTCACTCCCAAGATGTCTGGAGACAGTTATATCTGTGGAGACAGTGTGCG	7904

Db	9153	TGAGGTTCTCTTAATGCAAGTCTGTGCTGTGGCCAGAAAGTATACTTTTGGGCTTACTGTTTCA	9212
QY	7905	GTAACAGTGCATCGGCAAGCGTACTCTGGTGGGAAACAGACCCGATGTGGCGTGA	7964
Db	9213	CTATTCTGCAAGAAAGGTTCCCTTTAAGCCAGTCATCAAGAACTCGCCAAATTGAA	9272
QY	7965	TGGAACATGGACATGCGTCCCTCCCTCACTGCTCAGAAACACAGCTGGAGTTTGGGGTGA	8024
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QY	8025	CCCTGGGATCCCGGCTCATGGACCTCCGTTTGGGGGACAAGCTTTGATCCAGCACTGTGAT	8084
Db	9333	TCCAGGTAATCTCCGGCCATGGCTCTTGAACAGAAAGCAATTTCAAGAACTTAAAGTACTGT	9392
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QY	8445	GTTGTGCTCCGTGCTATATGATGAGTCACATAGAGTATGTGTGAGCTGACCAAGGA	8504
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QY	8505	CCGGAACATGGAATGGAACCAAGCCGCTGTGCAAAAGCTCTCATGTGACACCACTCCGT	8564
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QY	8565	CATCCCAATGGGAAGGTGGTGGGGTGTGACTTCATGTGGGGCTCAAGTGTACTTATGC	8624
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RESULT 15  
 AY017307

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 10944)  
 Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B.  
 Transcription map of the 8p23 putative tumor suppressor region  
 Genomics 75 (1-3), 17-25 (2001)  
 MEDLINE 21365705  
 JOURNAL 2 (bases 1 to 10944)  
 PUBLISHED 11472063  
 REFERENCE 2 (bases 1 to 10944)  
 Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B.  
 Submitted (08-JAN-2001) Otolaryngology, Washington University  
 School of Medicine, Box 8115, 517 S. Euclid Ave, Saint Louis, MO  
 63110, USA  
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## ORIGIN

Query Match 33.4%; Score 3387.8; DB 9; Length 10944;

Best Local Similarity 61.2%; Pred. No. 0;

Matches 6056; Conservative 0; Mismatches 3187; Indels 646; Gaps 11;

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QY	460	ATTGATGATGACAAATGACATGCTGTGTGATCATCATCAGACTCAACCCCTCAG	519
DB	1573	GTTCAAGTAAAGATTAATGACATCTGTGTGTGGTCAATCAACACGACCCGGAAG	1632
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DB	1633	GTCATCAAGCTTGCTTTGAGAGGTTTGAAGTGTGAGCGAGCTATGACACCTTGAGT	1692
QY	580	GGTGATGTGTGATGAGTAGGAGCAAGAAAGACAGTTCTTACATGTCTTAAATGCTGC	639
DB	1693	GGTGTGTGTGGAGAGGTGGAGAACACAGATCGGTCTTGTACGTG-----	1737
QY	640	AGTGAAGAGCTCAACCCGAGGCTCTGCATCCAGAGAGAGATGTCTGGGACATGG	699
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DB	1780	AACCAAGTGTGCTACATCTGSCAGTCGAGTATAGCATTTGGC-----	1821
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QY	940	GGAAGAGGAATCAATGCAATGCAAAAGATTAACCAATGCTGGGTAAGAACGAGCTGC	999
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QY	1360	GGCTTCCAGTAATATGCAACGCTTTGGGAGCAGCTTCCAGTGGGCACTCATCTCC	1419
DB	2389	GGCATTCCTAATAAGAGACAGCTTTGGTGAAGGTTTCACTCGGAGCTCGGTTCT	2448
QY	1420	TTCCTGTGATGAAGCTTCTTGGGACTCAGGCTCAGAGCATTAATCTGCTGCTG	1479
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QY	1480	AAGAGGGCAGCGGTGTGGAACAGCGCTGTGCGGGTGAAGCTCCGTTGGTGT	1539
DB	2509	CAAGCGGAAACGAGTGTGAGCTCCACGCTGCCCGCTGGAAGCTCAATGTGTGA	2568
QY	1540	CACCTGACTTGGCCAGCGGACCATCTCTCCGAGCTGGCTGAGCTTTCATCAAGAT	1599
DB	2569	CATCTGAGAGGCTCAGGAGGATCATTTTGTCTCTGAGTGGCAGAGTATTAAGAT	2628
QY	1600	GCTTGAAGTGTGCTGGGTGATGAGGCCAGGAGCTTACCCATCAATAATCACTTC	1659
DB	2629	TCTTACATGTGTGATGATTAATGAAGCAAAACAGGCACTCATCAATAATGACTTTT	2688
QY	1660	GACAGATTCAAAACCGAGGTCAATTAAGACCCCTGGAAGTAAGGAGGCGGACTTAC	1719
DB	2669	GACAGATTTCAGACAGAGTAATTAATGAACCTTGAAGGTCAGAGAGGCGCAGCAGT	2748
QY	1720	TCAGGCGCTTGAATGGGGTTTACAGAGGAGCCAGGTTCCCACTTCTCATGACAGC	1779
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Db	2869	ATCCACTATGAGAGGTGACCGCTTGAGTCGGATTCCTGGCTGGACCCGGGATCCCTGTG	2928
OY	1900	AATGACAGCGCTCAATGGGAATGACTTCTTCACTGGGCGCGCTGGAGACCTTCAGCTGTGAC	1959
Db	2929	AACGGCCATCGCCACGATGAGACTTTGGCATCAAGTTCACAGTACCTTTCAAGCTGTGAC	2988
OY	1960	TCGGGCTACACATTTAAAGTACGGGGAGCCTCTGGAGTGTGAGCCCAATCTTCAGTGGAGC	2019
Db	2989	CCGGGGTACACACTTAAGTACGACGAGCCCTCGTGTGTGAGAGAAACACCAATGGAAAC	3048
OY	2020	CGGGCCCTCCCACTTTGTAAGCTCTCTGTGTGGCTTCAATCAAGGCTCCAGTGGAGC	2079
Db	3049	CACGCTTTGCCAGCTGTGACGCTCTTAATGTGAAGCTACATCCAAAGGAAAGTGGAAACA	3108
OY	2080	ATCTTGTGCGAGGGTTCCTCGACTTCACCCCAACCTTGAATCGACCTGGATTAATC	2139
Db	3109	GTCTCTTCTCTGGGTTTCCAGATTTTATCCAACTCTTAACATGACGTGGACATTT	3168
OY	2140	GAACATCTCATGCGCAAGGTGTGTCTTCCACTTTCACACTTTCACCTTGAAGTGGC	2199
Db	3169	GAAAGTCTCATGGAAGAAAGATTCATTAATCTTTACACACTTTCATCTTGAAGATTC	3228
OY	2200	CATGACTACCTCTTCATCACTGAGAACGGACGCTTACCCAGCCCTCGAGGCACTAAT	2259
Db	3229	CACGACTATTACTGATCACAAGAGATGGAAGTTTTTCCGAGCCCGTGGCCAGGCTCAC	3288
OY	2260	GGATTCGGGCTGCGCAGCTCCATCAGCGCTGGGCTCTATGGCACTTTCACCTGCCAGTCT	2319
Db	3289	GGGTGCGTGTTCCTCATACGATCAAGGACAGCCGTGTGGAAACCTTCACCTGCCACCTT	3348
OY	2320	CGCTTCATCTCTGATTTCTCCATGTCATATGAAGATCAACATCACTTCTCAGAGTAC	2379
Db	3349	CGGTTTATATCAGACTTCTCAATTTCTGACAGGGCTTCAATATCACATTTTCAGATAT	3408
OY	2380	GACTTGAAGCCCTGTGAGAGCCGAGGTCCAGGCTACAGCATTCGGAAAGGCTTGACG	2439
Db	3409	GACCTGGAGGCATGTGATGATCTGTGAATCCCTGGCTTCAACCGAAGAAATGGTTTTCAC	3468
OY	2440	TTTGGCGTGGGCGACACTTGAACCTTCTCTGCTTCCCGGGTACCGTCTGAGGGCAC	2499
Db	3469	TTTGTGTGGGAGACTCTCTGACGTTTTCTCTGCTTCTGGGATATCGTTTGAAGGTGCC	3528
OY	2500	GCCGCGCATCAGGTGCTGGGGGGGCGAGAGGGCGCTGTGGAACTGCGCTCGCCCAAGGCT	2559
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OY	2560	GTTGCTGAGTGTGGGAATTCAGTCCACAGCACTCAGGGTACTTTGTCTGTCCCAACTTT	2619
Db	3589	GTTGGCGGATGTGGAGCAAGTGTCAAAGGAATGAAGAACATTATCTCTCCAAATTTT	3648
OY	2620	CCTGTGAACCTAACATATCATGATGATCTACTCCATCCAGACCCAGCCAGGAAG	2679
Db	3649	CCATCCCAATTATGATAATACCATGAGTGTATCTATAAATAAGAAACAGAAGCCGCGAAG	3708
OY	2680	GGAATTCAGCTGAAAGCCAGGGCACTTGGAACTCTCCGAAGAGATGTCTCAAGTTTAT	2739
Db	3709	GGCAATCCACCTTGAACACGAAGCTTCCAGCTGTTTGAAGAGATATCTTAAAGATAT	3768
OY	2740	GATGGCAACAACAATCCGCGCGGTGTGCTGGAGATTTTATGCACTTGAATGATGGCG	2799
Db	3769	GATGAAAAAGACAGTTCTCTCAGCTCACTGGGCAAGTTCATMAAAATGAACCTTGTGGG	3828
OY	2800	GTGACTTTGAACAGACATCCAGCAGTGTGTGGCTTGAATTCATCACTGATGTGAANA	2859
Db	3829	CTGATCTTAACAGCACAATCCAAATCACTAATGGCTAAGATTCAACCAATGATCTGAC	3888
OY	2860	ACCAAGCAAGGCTTGAATGCACTTTTCAGCTTGAATCTCAATCAATGTGAAGACCA	2919
Db	3889	ACCGACCAAGTTTTTCACTCACTATACAGTTTTGATCTGGTAAATATGAGAGATCCG	3948

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QY	2980	TCTTTCAGCTGTGACCCCTGGAATACAGCTCGGGGGTAGTAGAGACTGTGTGTCTGAGT	3039
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QY	3040	GGAGAGCGCCGGACCTTGGGACCGGCCTCTGCCCCACTGTGTGCGCGAGTGTGGAGGACA	3099
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Db	4249	ATTGTTTTGCACGGAGATGGCTTCACGACATCTCAAGAGTGTGGAGCGGGCGGTGGAC	4308
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Db	4309	AGTGACATCTCTGTGAAGAGAGTGAAGTGTGCTCCGCCCTTCGGAGGACATCCACAGCAC	4368
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Db	4609	CAACCAAGACCTCTCTACATGTAGTAGTCTGTGTGAGGGAATCTGACGGGCGACAGAGT	4668
QY	3640	GTCATCTCTCAACCAATTATCCCAAGACCTTACCCGCGCAGGACAGAGATGTGACTGAA	3699
Db	4669	GTTATTTTGTCAACCACTACCCACAGCGGTATCTCTCGGAAAGAAATGTGACTGTGAGA	4728
QY	3700	GTGACCGTCTACCAAGACTAGGTATGTGCTGCTGTGATTAATCACTTTAACCTGGAGCT	3759
Db	4729	GTAAGAGGAAACCGGACTTTTGTATGTGCTTGTATTAATCAAAAGTTTCAATGAGGCC	4788
QY	3760	GGCTATGACTTCTTCCATATCTACGACGAGACTCTCTCAGCCCTCTCATAGGAAGC	3819
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QY	3820	TTTATAGGCTCCCAAGCTCCAGGCGCATTTGAAAGCAGACGAACAGCTTCTCTGTGCC	3879
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QY	3880	TTTCGCAAGCATGTCTGTGAGCAATGCTGGCTTCTGTCAATTTGACTATACGAAAAACCG	3939
Db	4909	TTTCGGAATGATGCTCTCGTGGGCTTTTCAAGGTTTCGCAATTTTAAAGAGAAACCA	4968
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Db	4969	CGGGAAGCTTGTTTGACCCAGAAATTAATGATTTGAGGACAAAGTTTGGAAACAGACTTC	5028
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Job time : 27655 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: October 18, 2004, 10:04:46 : Search time 507 Seconds

(without alignments)  
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Title: US-10-016-248-1

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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112.4	1.1	10878	4	US-09-911-842A-1
2	100.8	1.0	11230	4	US-09-911-842A-3
3	100.6	1.0	63588	4	US-09-873-404-3
4	100.6	1.0	63588	4	US-10-243-735-3
5	100.6	1.0	168174	4	US-10-071-411A-63
6	100.6	1.0	168273	4	US-10-071-411A-2
7	99.8	1.0	349	4	US-09-513-999C-36203
8	99	1.0	162450	3	US-09-345-882-1
9	98.2	1.0	346	4	US-09-513-999C-10089
10	98	1.0	183	4	US-09-513-999C-9448
11	97.4	1.0	64467	4	US-09-803-671B-3
12	97.2	1.0	318	4	US-09-513-999C-28495
13	96.4	1.0	322	4	US-09-513-999C-16959
14	94.8	0.9	116592	4	US-09-818-512-3
15	94.8	0.9	786431	4	US-09-751-389-3
16	93.2	0.9	32042	3	US-09-245-281-44
17	93.2	0.9	32042	4	US-09-340-620A-63
18	93.2	0.9	40328	3	US-08-742-185-102
19	92.4	0.9	193303	4	US-09-497-855A-37
20	92.4	0.9	193303	4	US-09-497-855A-44
21	91.6	0.9	168174	4	US-10-071-411A-63
22	91.6	0.9	168273	4	US-10-071-411A-2
23	91.6	0.9	254366	4	US-09-822-871-3
24	91.4	0.9	403	4	US-09-621-976-8908
25	91	0.9	404	4	US-09-621-976-19332
26	90	0.9	270	4	US-09-621-976-1861
27	90	0.9	411	4	US-09-513-999C-23339

28	87.8	0.9	128779	4	US-09-497-855A-38	Sequence 38, Appl
29	87.6	0.9	409	4	US-09-513-999C-12046	Sequence 12046, A
30	87.6	0.9	447	4	US-09-621-976-9338	Sequence 9338, Ap
31	87.4	0.9	239	4	US-09-513-999C-10170	Sequence 10170, A
32	86.2	0.9	452	4	US-09-621-976-7867	Sequence 7867, Ap
33	85.4	0.8	1223	4	US-09-461-325-101	Sequence 101, App
34	85.4	0.8	1223	4	US-10-012-542-101	Sequence 101, App
35	85.4	0.8	1223	4	US-10-115-123-101	Sequence 101, App
36	84	0.8	7505	3	US-09-078-294-13	Sequence 13, Appl
37	82.8	0.8	102	4	US-09-513-999C-29514	Sequence 29514, A
38	82.8	0.8	1757	4	US-09-489-847-12	Sequence 12, Appl
39	81.8	0.8	392000	4	US-10-027-983-11	Sequence 11, Appl
40	81.4	0.8	168575	4	US-09-426-290-1	Sequence 1, Appl
41	80.6	0.8	323	4	US-09-621-976-9481	Sequence 9481, Ap
42	79.8	0.8	786431	4	US-09-751-389-3	Sequence 3, Appl
43	79	0.8	544	4	US-09-370-838-280	Sequence 280, App
44	79	0.8	544	4	US-09-654-133-280	Sequence 280, App
45	78.8	0.8	3461	4	US-10-140-002-199	Sequence 199, App

## ALIGNMENTS

RESULT 1	US-09-911-842A-1	Sequence 1, Application US/0911842A
Patent No. 6656707		
GENERAL INFORMATION:		
APPLICANT: Amgen Inc.		
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF		
FILE REFERENCE: 01017/37592		
CURRENT APPLICATION NUMBER: US/09/911,842A		
CURRENT FILING DATE: 2001-07-24		
PRIOR APPLICATION NUMBER: US 60/222,438		
PRIOR FILING DATE: 2000-08-01		
NUMBER OF SEQ ID NOS: 7		
SOFTWARE: PatentIn version 3.0		
SEQ ID NO 1		
LENGTH: 10878		
TYPE: DNA		
ORGANISM: Homo sapiens		
US-09-911-842A-1		
Query Match	1.1%	Score 112.4; DB 4; Length 10878;
Best Local Similarity	45.4%	Pred. No. 3.2e-20;
Matches 560; Conservative	0;	Mismatches 641; Indels 33; Gaps 3;
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DB	8028 CAACTTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	8087
QY	7046 GCCAAGGATCATCCCTGTCAGGCCAATGCAATGAGACCTGGGGACTTACGCCA	7105
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QY	7586	CCCAATGCTGGCCAGCGGGGCAATGGATGTGACATGCTGCCCACTGCAAGATCATCAACT	76450
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QY	7646	GTACAGATCTGAGCACCCAGAAATAATGTGTTCGTCAAGTCCAGCTCCAGCCAGCGGCCGACAA	77050
Db	8682	GTGCCACCCCGCAACATGTGGCAATGGGGATGACGGAAGGCTGTGATATGGC-----	8734
QY	7706	GGTTCAGCTTGGGCAACACTGTGTTCACCGGTGAACCAACGCTTCTTACTCTCTGGGCA	7765
Db	8735	-----TTCATGAGGAAGTAACTTTCACCTGTCAAGAGAGGGCTACTCTTGGACGGTG	8786
QY	7766	CCCCAGTCTCAGCTGCCAGGAGATGGCAATGGGACCGTCCCGGCCCCAGTCTCT	7825
Db	8787	CTCCAAAATCACTGTGATGATGATGAGCACTGGAGTGCAGAGATTCCTCTGTGAAAC	8846
QY	7826	TGTGTCTCTGTGGCCATCCGGGCTCCCGCTCACTCCAGATGTCTGGAGACATTATA	7885
Db	8847	CAGTCAATGTGTGACCTCTCAAGATCTTGGCCCATGGTTTCCCTAATGTTCCTTTA	8906
QY	7886	CTGTGGGAGCAGTGTGTGGGTACAGCTGCATTCGGCAAGCTATCTGTGGAAATACGA	7945
Db	8907	TTCAATGGGGCCATATATACATGATCAGTCTTTCCTGTATTAATCACTCANTGAAATTCAT	8966
QY	7946	CCCGCATGTGTGGGCTGGATGAGACACTGGCTCCCTCCCTCACTGCTCAGGAACCA	8005
Db	8967	CAAGAAGT-----GCTCTTCATATGGCTCCTGGAGTGGCAGTCACTTCTCT	9014
QY	8006	GCGTGGGAGTTTGGGCTGACCTCTGGGATCCGGGCTCATGCGATCCGTTTGGGGAGCAGT	8065
Db	9015	GCCGTGCTTGCAGATGTTCCACACACAGTAATTTGAATATGGAACGTCAATGGGACAGATT	9074
QY	8066	TTGATTCACAGCAGCTGTGATGCGCTTCAAGCTGTGAAGCTGGGCAAGTCTCCGGGATCGT	8125
Db	9075	TTGACTGTGGAAAGGCAAGCCCGGATTCAGTCTTCAAAAGGTTTCAAGCTCTTAAAGACTTT	9134
QY	8126	CAGAGCGCACTGTCAAGCCCAATAGCTGTGGAGCGGCTCGCAAGCTGAGTGTGAGATGA	8185
Db	9135	CTGAATATCACTGTGAAAGCCGATGGCCAGTGGAGCTCTGGGTTTCCCCCACTGTGAACAA	9194
QY	8186	TCTCTGTGGGAACCTCTGGGACTCTCAAGTATATGC	8219
Db	9195	CTTCTGTGTGTTCTCTTCATATGATTAACCAATGC	9228

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RESULT 2
US-09-911-842A-3
; Sequence 3, Application US/09911842A
; Patent No. 6658707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842A
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 3
; LENGTH: 11230
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-911-842A-3

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Query Match	1.0%;	Score 100.8;	DB 4;	Length 11230;
Best Local Similarity	45.6%;	Pred. No. 6e-17;		
Matches 409; Conservative	0;	Mismatches 472;	Indels 15;	Gaps 1

QY	7100	CGCCCACTGCGCGAATCATCTCCGTGTGAGAGCTCCGATTTCCGCCCAATGGCCACCGCA	7155
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QY	7160	TCCGACACTGTCTGTCTACGGGGCAACAGCCATCTTCTCCTCGCAATTTCCGGATACACAC	7219
Db	8352	ATTTCACACAGACACTATGTGGCGAGTGTGCACATATATAGCTGCAGCGGGGACATTC	8411
QY	7220	TGGTGGGCTCCAGGGTGCCTGTGAGTGCATATGGCCATATGGGCTCTGGATGTGCTCTGAAGTCC	7279
Db	8412	TAGAGGCTCCCACTTAAGACTCTGTCTGCGAATAAGACAGTGAAGTGGCACTGTTCAC	8471
QY	7280	GCTGCCCTTGTGCGACACTGTGGGACTCTGTAGAGCCCATTTGTCAACGGAACACATCAATGGGG	7339
Db	8472	GCTGTGAAGCCATCTCATGTGACGTAAAGCCAAACCCACTGTGGAAATGCATTCATAAGAG	8531
QY	7340	AGAACTACAGCTACCGGGGACAGTGTGGTGTATCCATATGCATATGCTGCTTCCGCTATGCT	7399
Db	8532	ATGACTACTCTCTACCTGGGGTGTATATACACGAGTGTGACTCTGGGCTATATTTCTCATG	8591
QY	7400	GCAATGTGTGGCCATCTGCACAGAGATCATCACTGCTGGGCAAGACCCCTTTCTGTG	7459
Db	8592	GCTCTAAGAAAGAGACATGECCAAGAAATATGAATTTGGATGGGCAATGAGCCCATGTGT	8651
QY	7460	TGCCAATTACCTGTGACACCCAGGCAACCTGTCAACGGCTCTACTCAGGGTAACAGT	7519
Db	8652	TTCTGTGAGCTGTGGCTCACCCCAAGTCCCCACCAATGACCGAGTGAAGGGAAGAAAT	8711
QY	7520	TTTAACTCAACATATGTGTCAAGTTGTGTGCAACCTGGGTATATGGCTGAGGGGCTG	7579
Db	8712	ACCACTTCCAAAGAGATTAACACTCTTGGCGGTGAAGGATTCATCTGAAAGAGCA	8771
QY	7580	CTAGTCCCAATGCTGTGGCAGCGGCAATGAGTGCATAGCTGCCCCACCTGCAGAAATCA	7639
Db	8772	GAGTGTGTATCTGTCTTACCAATAGGAATTTGGATGGTGCACATCCAGCTGCATGTCTG	8831
QY	7640	TCACTGTACATATCTGTGACACCAAGAAATATGTGTTGCTCAGGTCAAGCCAGCGGC	7699
Db	8832	TTTGAATGTCTGTGCCCAACCAAGTGTCCAAATGGGGTGGACATGTGCTTGAC-----	8884
QY	7700	CGCACAGTTCAAGCTTTCGGCACCACTGTGTCTTAACGGTCAACACAGGCTTTCACTGC	7759
Db	8885	-----TATGGGTTCAAGAAAGAAAGTATGCTTTCACATGTTCAAGAGGCTATGTGCTGC	8936
QY	7760	TGGGCAACCCCACTGTCTAGTGTCCAGAGGAGATGACATGGACCGTCCCGCCGCCAGT	7819
Db	8937	AGGGGGCTCCAAACATCACCTGTCACTCCAAATGGGACTTGGATGACAGAAATCCCTGTCT	8996
QY	7820	GTCCTTGGGTGCTGTGGCCATCCGGGGCTCCCGGCTCATCTCCAGATGTCTGGANACA	7879
Db	8997	GTTAAACAGTACCTGTGTGCTCTCTGCGGACCTTCCCAAGGGCTTCCCTAAATGGCTTTT	9056
QY	7880	GTTATATCTGTGGAGACATGTGTGGGTATACAGTGCATTCGCAAGCTACTCTGGTGGAA	7939
Db	9057	CTTTTATCATGGGGGCCACATACAGTATACAGTGTTTACTGGTTATTAACCTTATGGA	9116
QY	7940	ACAGCACCCGCACTGTGTGGCTGTGATGACATCTGACTGTGCTCTTCCTCATCTGC	7995
Db	9117	ACCACTCAAGAAATGCTTTCCAATGATGTCTCGAGCGGCACTGCGCATCTCTGC	9172

RESULT 3  
US-09-873-404-3/c







[illegible]

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NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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Best Local Similarity 95.3%; Pred. No. 1.2e-15;
Matches 102; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Oy 10090 CTGCGTAGCCTGCCGAGTGCCCTGCAGATTGCAGCGCGGACGCCACC 10136
Db 19845 CTGCGTAGCCTGCCGAGTGCCCGGCGATTGCAGGTGCGGCGTGCAC 19799
RESULT 9
US-09-513-999C-10089
Sequence 10089, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
Ductert, A.
Giordano, J.Y.
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RESULT 13  
US-09-513-999C-16959  
; Sequence 16959, Application US/09513399C  
; Patent No. 6783961  
; GENERAL INFORMATION:

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? APPLICANT: Dumast Milne Edwards, J.B.
? APPLICANT: Duclert, A.
? APPLICANT: Giordano, J.Y.
? TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
? Patent No. 6783961
? FILE REFERENCE: 59, US2.REG
? CURRENT APPLICATION NUMBER: US/09/513,999C
? CURRENT FILING DATE: 2000-02-24
? PRIOR APPLICATION NUMBER: US 60/122,487
? PRIOR FILING DATE: 1999-02-26
? NUMBER OF SEQ ID NOS: 36681
? SOFTWARE: Patent.pm
? SEQ ID NO 16959
? LENGTH: 322
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-513-999C-16959

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						Gaps	0

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 Db 19 ATGCGGGGGCGCCCTCCCGCAGCTCGCTGCGCGCTTGACGTTGATCTCAGACTGCTGT 78

Oy      61 GCTAGCAATCAGCGACACTCCGTGGGCGTAGAACCTCCGAGCTAG    106  
       ||| | | | | | | | | | | | | | | | | |  
Db      79 GCTGGCAATCAGCGAGACTCCGTGGGCGTAGAACCCTCCGAGCCAG    124

RESULT 14  
US-09-818-512-3

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: Sequence 3, Application US/09818512
: Patent No. 6537780
: GENERAL INFORMATION:
: APPLICANT: BEASLEY, Ellen et al.
: TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CL001192
: CURRENT APPLICATION NUMBER: US/09/818,512
: CURRENT FILING DATE: 2001-03-28
: NUMBER OF SEQ. ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 116592
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(116592)
: OTHER INFORMATION: n = A,T,C or G
: US-09-818-512-3

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QY 61 GCTAGCAATCAGCAGACTCCGTTGGCGGTAGAACCTCCAGCTAG 106  
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Db 54159 GCTAGCAATCAGCAGATTCGTTGGCGGTAGAACCTCCAGCTAG 54204  
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RESULT 15
US-09-751-389-3/C
; Sequence 3, Application US/09751389
; Patent No. 6610334
; GENERAL INFORMATION:

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? APPLICANT: GUEGLER, Karl et al
? TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
? TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
? TITLE OF INVENTION: THEREOF
? FILE REFERENCE: C0001067
? CURRENT APPLICATION NUMBER: US/09/751,389
? CURRENT FILING DATE: 2001-01-02
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 786431
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc.feature
? LOCATION: (1)..(786431)
? OTHER INFORMATION: n = A,T,C or G
? US-09-751-389-3

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QY 61 GCTAGCATCAGCGACACTCCGTGGCGTAGACCCCTCCAGCTAG 106  
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Db

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Job time : 514 secs

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Job time : 514 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: October 19, 2004, 02:09:49 : Search time 2932 Seconds

(without alignments)  
17684.649 Million cell updates/sec

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Perfect score: 10136  
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Gapop 10.0, Gapext 1.0

Searched: 3403857 seqs, 255783690 residues

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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	7616.4	75.1	8010	16	US-10-016-248-3
3	4260.4	42.0	6004	16	US-10-016-248-38
4	2715.4	26.8	7333	15	US-10-016-248-38
5	2715.4	26.8	8034	15	US-10-016-248-38
6	2671	26.4	6409	15	US-10-016-248-38
7	2503.6	24.7	5598	15	US-10-016-248-38
8	2450.8	24.2	5667	15	US-10-016-248-38
9	2450.2	24.2	6145	15	US-10-016-248-38
10	2122.4	20.9	2487	9	US-09-799-514-3
11	1569	15.5	3810	16	US-10-108-260A-814
12	1442.8	14.2	4506	16	US-10-016-248-27
13	1371.6	13.5	2387	17	US-10-016-248-69

14	1031.2	10.2	1615	16	US-10-451-010-20	Sequence 20, Appl
15	783.6	7.7	2609	17	US-10-399-455-31	Sequence 31, Appl
16	594.8	5.9	894	15	US-10-243-552-196	Sequence 196, Appl
17	585.4	5.8	3145	16	US-10-114-270-31	Sequence 31, Appl
18	557.6	5.5	3726	16	US-10-108-260A-533	Sequence 533, Appl
19	488.6	4.8	1338	16	US-10-016-314-64	Sequence 64, Appl
20	440	4.3	458	9	US-09-833-381-1919	Sequence 1919, Appl
21	419.2	4.1	1581	11	US-09-764-875-235	Sequence 235, Appl
22	414.2	4.1	427	15	US-10-243-552-779	Sequence 779, Appl
23	404.4	4.0	442	10	US-09-918-995-28608	Sequence 28608, Appl
24	327	3.2	344	9	US-09-864-761-29585	Sequence 29585, Appl
25	327	3.2	542	9	US-09-864-761-13022	Sequence 13022, Appl
26	269.4	2.7	321	9	US-09-764-881-35	Sequence 35, Appl
27	269.4	2.7	321	9	US-09-764-853-196	Sequence 196, Appl
28	269.4	2.7	321	10	US-09-764-875-525	Sequence 35, Appl
29	269.4	2.7	321	11	US-09-764-875-525	Sequence 525, Appl
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31	234.4	2.3	1992	9	US-09-729-674-91	Sequence 91, Appl
32	204	2.0	507	9	US-09-864-761-6782	Sequence 6782, Appl
33	203	2.0	203	9	US-09-864-761-23515	Sequence 23515, Appl
34	192.2	1.9	551	9	US-09-864-761-12509	Sequence 12509, Appl
35	192	1.9	339	9	US-09-864-761-29076	Sequence 29076, Appl
36	190.4	1.9	330	13	US-10-027-632-42652	Sequence 42652, Appl
37	190.4	1.9	330	15	US-10-027-632-42652	Sequence 42652, Appl
38	184.4	1.8	515	9	US-09-864-761-13078	Sequence 13078, Appl
39	181.4	1.8	183	9	US-09-864-761-29639	Sequence 29639, Appl
40	179.4	1.8	1084	13	US-10-027-632-10845	Sequence 10845, Appl
41	179.4	1.8	1084	13	US-10-027-632-10846	Sequence 10846, Appl
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43	179.4	1.8	1084	15	US-10-027-632-10845	Sequence 10845, Appl
44	179.4	1.8	1084	15	US-10-027-632-10846	Sequence 10846, Appl
45	179.4	1.8	1084	15	US-10-027-632-10847	Sequence 10847, Appl

## ALIGNMENTS

RESULT 1  
US-10-016-248-1  
Sequence 1, Application US/10016248  
Publication No. US20040033491A1  
GENERAL INFORMATION:  
APPLICANT: Alsbrook et al.  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-218  
CURRENT APPLICATION NUMBER: US/10/016,248  
PRIOR FILING DATE: 2002-09-20  
PRIOR APPLICATION NUMBER: 60/254,329  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/291,037  
PRIOR FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: 60/255,648  
PRIOR FILING DATE: 2000-12-14  
PRIOR APPLICATION NUMBER: 60/297,173  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: 60/309,258  
PRIOR FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/326,393  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/315,639  
PRIOR FILING DATE: 2001-08-29  
NUMBER OF SEQ ID NOS: 167  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 10136  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-016-248-1  
Query Match 100.0% Score 10136, DB 16, Length 10136,  
Best Local Similarity 100.0% Pred. No. 0,  
Matches 10136, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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Db 2761 CGTTTGCTGGGAGTTTATAGCCATTCTGAGATGATGGGGGTGACTTTGAAACAGCACTCC 2820  
Qy 2821 AGCAGCTGTGGCTGATTTCATCACTGATGCTGAAACCCAGCAAGGGCTTTGAACCTG 2880  
Db 2821 AGCAGCTGTGGCTGATTTCATCACTGATGCTGAAACCCAGCAAGGGCTTTGAACCTG 2880  
Qy 2881 CATTTTCCAGCTTTGAACTCATCAATGTGAGAACCCCAAGTTTGCTGAC 2940  
Db 2881 CATTTTCCAGCTTTGAACTCATCAATGTGAGAACCCCAAGTTTGCTGAC 2940  
Qy 2941 AAGGTTCAATGATGAAAGTCAATTTGCAAGGAGCTCCGTCTCTTCACTGTGACCTTGA 3000  
Db 2941 AAGGTTCAATGATGAAAGTCAATTTGCAAGGAGCTCCGTCTCTTCACTGTGACCTTGA 3000  
Qy 2941 AAGGTTCAATGATGAAAGTCAATTTGCAAGGAGCTCCGTCTCTTCACTGTGACCTTGA 3000  
Db 2941 AAGGTTCAATGATGAAAGTCAATTTGCAAGGAGCTCCGTCTCTTCACTGTGACCTTGA 3000  
Qy 3001 TACAGCTGTGGGATGATGAGAGCTGTGTCTGAGTGAAGGCGCGGACCTTGGAG 3060  
Db 3001 TACAGCTGTGGGATGATGAGAGCTGTGTCTGAGTGAAGGCGCGGACCTTGGAG 3060  
Qy 3061 CGGCTCTTCCCACTGTGTGCGCGAGTGTGAGAGCAGTGAAGAGAGGTGTGGAG 3120  
Db 3061 CGGCTCTTCCCACTGTGTGCGCGAGTGTGAGAGCAGTGAAGAGAGGTGTGGAG 3120  
Qy 3121 CAGGTCTGTCAACCGGGGTATCCAGTCCCTATGAAACAATCTCAACTGCACTGTGAGAC 3180  
Db 3121 CAGGTCTGTCAACCGGGGTATCCAGTCCCTATGAAACAATCTCAACTGCACTGTGAGAC 3180  
Qy 3181 ATCGAAGCAGAGCGCGGTGACCATTTGGGCTACCTTCTGCTGTTTGAACAGAGAG 3240  
Db 3181 ATCGAAGCAGAGCGCGGTGACCATTTGGGCTACCTTCTGCTGTTTGAACAGAGAG 3240  
Qy 3241 GTTCAAGAGTGTGCGCATCTGGAGTGGGCTGTGAGAGCGGGGTTCTGCTGAAGAG 3300  
Db 3241 GTTCAAGAGTGTGCGCATCTGGAGTGGGCTGTGAGAGCGGGGTTCTGCTGAAGAG 3300

Qy 3301 CTGAGTGGCCGGGCTCTGCGCAAGGACCTGATAGCACTTGAACCTGGTGGCTGAG 3360  
Db 3301 CTGAGTGGCCGGGCTCTGCGCAAGGACCTGATAGCACTTGAACCTGGTGGCTGAG 3360  
Qy 3361 TTCAAGCACTGATCTTTCACACGAGCAGGCTTTGCCATTCAATTTTCAAGTGTGACA 3420  
Db 3361 TTCAAGCACTGATCTTTCACACGAGCAGGCTTTGCCATTCAATTTTCAAGTGTGACA 3420  
Qy 3421 GCAAGCTCTGCAATGACCTTGGATCCCGCAATGGAGTGGAGTGTGACAGTTGG 3480  
Db 3421 GCAAGCTCTGCAATGACCTTGGATCCCGCAATGGAGTGGAGTGTGACAGTTGG 3480  
Qy 3481 GAAAGCGGAGCTTCCAGAGTGTGACAGTGTGACCGCTGAGCGCTGAGGGAAGTGA 3540  
Db 3481 GAAAGCGGAGCTTCCAGAGTGTGACAGTGTGACCGCTGAGCGCTGAGGGAAGTGA 3540  
Qy 3541 GAGATCAGCTGTGTGAAGATCGAAGAACAGTTCCTTGTGACAGCCAGCCGCAACATG 3600  
Db 3541 GAGATCAGCTGTGTGAAGATCGAAGAACAGTTCCTTGTGACAGCCAGCCGCAACATG 3600  
Qy 3601 ATGCTCTCTGCGGGGAGACCTGACAGGACCATCTGAGTATCTTCAACCAATTAC 3660  
Db 3601 ATGCTCTCTGCGGGGAGACCTGACAGGACCATCTGAGTATCTTCAACCAATTAC 3660  
Qy 3661 CGAAGACCTTACCCGACAGGAGAGTGTGACTGGAAGTGAACGCTTCAACAGACTAC 3720  
Db 3661 CGAAGACCTTACCCGACAGGAGAGTGTGACTGGAAGTGAACGCTTCAACAGACTAC 3720  
Qy 3721 GTCAATGCGCTGTATTTAATCACTTTAATCTGAGCTGGGCTGATGACTTCTCATATC 3780  
Db 3721 GTCAATGCGCTGTATTTAATCACTTTAATCTGAGCTGGGCTGATGACTTCTCATATC 3780  
Qy 3781 TACGACGAGCGGACTCTCTACGCTCTCATAGGAAGTTATGCTTCCAGCTTCCA 3840  
Db 3781 TACGACGAGCGGACTCTCTACGCTCTCATAGGAAGTTATGCTTCCAGCTTCCA 3840  
Qy 3841 GGGCGGATTGAAAGCAGCAGCAACGCTCTTCTGCGCTTCCGACGAGTGTGATG 3900  
Db 3841 GGGCGGATTGAAAGCAGCAGCAACGCTCTTCTGCGCTTCCGACGAGTGTGATG 3900  
Qy 3901 AGCAATGCTGTGCTGTCAATGACTATACAGAAAAACCGCGGAGTCAATGTTTGAATCT 3960  
Db 3901 AGCAATGCTGTGCTGTCAATGACTATACAGAAAAACCGCGGAGTCAATGTTTGAATCT 3960  
Qy 3961 GGTTCATCAAGAACGAGCAGCGGCTGGCTCGACCTGAGCTGGGCTCTCCGTAC 4020  
Db 3961 GGTTCATCAAGAACGAGCAGCGGCTGGCTCGACCTGAGCTGGGCTCTCCGTAC 4020  
Qy 4021 TACTACTGCAAGGGGCTACGAAGTGAAGGACCTGACCTGAGCTGACCTTGGGG 4080  
Db 4021 TACTACTGCAAGGGGCTACGAAGTGAAGGACCTGACCTGAGCTGACCTTGGGG 4080  
Qy 4081 CCTGATGGGAACCGGTGTGAAACAATCCCGGACAGTGTGACAGCCCTGTGGGG 4140  
Db 4081 CCTGATGGGAACCGGTGTGAAACAATCCCGGACAGTGTGACAGCCCTGTGGGG 4140  
Qy 4141 CAGTATGAGGTTTCCAGCGAGTGTGTTGTCTCCCACTACCTCCAGAACTACACAGT 4200  
Db 4141 CAGTATGAGGTTTCCAGCGAGTGTGTTGTCTCCCACTACCTCCAGAACTACACAGT 4200  
Qy 4201 GGAAGATGCTGTGATTTTGTATTTTGTATCTGACCGCAAGACTATGTGTGTTGGCAATTC 4260  
Db 4201 GGAAGATGCTGTGATTTTGTATTTTGTATTTTGTATCTGACCGCAAGACTATGTGTGTTGGCAATTC 4260  
Qy 4261 GCTTCTTTCACACGCGCTTCAACGAGCTGTGAGGTTTCAAGCGGCTTGGCCAC 4320  
Db 4261 GCTTCTTTCACACGCGCTTCAACGAGCTGTGAGGTTTCAAGCGGCTTGGCCAC 4320  
Qy 4321 TCGCGGCTCTCAGCTCTCTCTGCGGCTCCATACAGGAGATCACTGCTTGGCCAC 4380  
Db 4321 TCGCGGCTCTCAGCTCTCTCTGCGGCTCCATACAGGAGATCACTGCTTGGCCAC 4380



Qy	4381	TCGAATCAAGTTGATTTAAGTTACAGCGCCAAAGCCTTGCAACAAGCCAGAGGCTTCCAC	4440
Db	4381	TCGAATCAAGTTCTCATTAATGATCAAGCGCCAAAGCCTTGCAACAAGCCAGAGGCTTCCAC	4440
Qy	4441	TTTGTTCAACCAAGCGGTTCTCTGCAACCAAGCGCCAGCAAGTGAAGTCTGTACCGGAAACC	4500
Db	4441	TTTGTTCAACCAAGCGGTTCTCTGCAACCAAGCGCCAGCAAGTGAAGTCTGTACCGGAAACC	4500
Qy	4501	CGCATATGGCAAGAGGCTGGGCAAGTGAATCTTGTGGTGGGGCCATCGTCCGTTGCAATGC	4560
Db	4501	CGCTATAGCAAGAGGCTGGGCAAGTGAATCTTGTGGTGGGGCCATCGTCCGTTGCAATGC	4560
Qy	4561	AACTCCGGCTATGCGCTGCAAGGAGTGCAGAGATCGAGTGCCTCCCTGTGCGCCGGGACC	4620
Db	4561	AACTCCGGCTATGCGCTGCAAGGAGTGCAGAGATCGAGTGCCTCCCTGTGCGCCGGGACC	4620
Qy	4621	TTGGGCCAATGGAAATCTCAAGCGCCACGATGTGGTGGCCGTGTGAGGCAACCTTCACA	4680
Db	4621	TTGGGCCAATGGAAATCTCAAGCGCCACGATGTGGTGGCCGTGTGAGGCAACCTTCACA	4680
Qy	4681	GAGCGGAGGAGGCAACATCTGCTGCTCCCTGCTCCAGAGCGATCCCTCAACAGCCCTCAAC	4740
Db	4681	GAGCGGAGGAGGCAACATCTGCTGCTCCCTGCTCCAGAGCGATCCCTCAACAGCCCTCAAC	4740
Qy	4741	TGTGTGTGAAGATGT	4800
Db	4741	TGTGTGTGAAGATGT	4800
Qy	4801	GTGACAGAGCAGAGCTGGGACTCGCTGGAAGTATTTGATGTGTGAGATTAACCTGTAAAC	4860
Db	4801	GTGACAGAGCAGAGCTGGGACTCGCTGGAAGTATTTGATGTGTGAGATTAACCTGTAAAC	4860
Qy	4861	ATGCTGGGGAGTTTCTCAGAAACAACCGTGTGCTGCTCTGAAACAGCACTTCAACAG	4920
Db	4861	ATGCTGGGGAGTTTCTCAGAAACAACCGTGTGCTGCTCTGAAACAGCACTTCAACAG	4920
Qy	4921	CTCTACCTTCACTTCTACAGATATCAGCGTATCTGACGTGCTTCACTGTGAGTAC	4980
Db	4921	CTCTACCTTCACTTCTACAGATATCAGCGTATCTGACGTGCTTCACTGTGAGTAC	4980
Qy	4981	AAAAAGGTGGGCTGAGAGATTTGTCGGAACTGTGTGCGCAATACGAGGTGAAAGT	5040
Db	4981	AAAAAGGTGGGCTGAGAGATTTGTCGGAACTGTGTGCGCAATACGAGGTGAAAGT	5040
Qy	5041	GCGGAGCGCTACTTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	5100
Db	5041	GCGGAGCGCTACTTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	5100
Qy	5101	CAGGGCCAGCGCCATCTCTGTGATGCTCCGGAACAGTCCGGCGATGGAATCACTCTCTCT	5160
Db	5101	CAGGGCCAGCGCCATCTCTGTGATGCTCCGGAACAGTCCGGCGATGGAATCACTCTCTCT	5160
Qy	5161	CAACTCTGTATGTGACAGTGTGGGGGAACAGTGAAGAGATGGAAGGGGTATCTCTGAGC	5220
Db	5161	CAACTCTGTATGTGACAGTGTGGGGGAACAGTGAAGAGATGGAAGGGGTATCTCTGAGC	5220
Qy	5221	CCCGGCTTTCCAGGCACTACCCAGTAACATGAGCTGCTCTGTGAAAAATAGCACTGCC	5280
Db	5221	CCCGGCTTTCCAGGCACTACCCAGTAACATGAGCTGCTCTGTGAAAAATAGCACTGCC	5280
Qy	5281	GTGGGCTTTGAGGTCATCCAGTTCTCGAACTTCTCAACCGAGCCCAACCAAGACTAC	5340
Db	5281	GTGGGCTTTGAGGTCATCCAGTTCTCGAACTTCTCAACCGAGCCCAACCAAGACTAC	5340
Qy	5341	ATTAAGAAATCCGGAATGAGCCCTTATGAGCAACCGCATGATGGAAGATTCAGTGAAGC	5400
Db	5341	ATTAAGAAATCCGGAATGAGCCCTTATGAGCAACCGCATGATGGAAGATTCAGTGAAGC	5400
Qy	5401	GAGCTTCAAGCTCCCTCTCTCAAGTGTGCAAGAGCAACCGTGTATTTTCCACAGGAC	5460
Db	5401	GAGCTTCAAGCTCCCTCTCTCTCAAGTGTGCAAGAGCAACCGTGTATTTTCCACAGGAC	5460
Qy	5461	CACCTCCAGAAATGCGCCAGAGATTCAGAGTATCAGAGCTTATGAACTTCAAGAGTGC	5520

Db 6541 TCAGCCCTTACTGACAGCTGCCAGGCGTCACTCCATGGCTTACTTACCTAGGCCAGACC 6600  
Qy 6601 AGACCCAGCCCGGGGCTCCATCCACTTTGGCTGCAACGCCCGGCTACCGGCTGGTGGGA 6660  
Db 6601 AGACCCAGCCCGGGGCTCCATCCACTTTGGCTGCAACGCCCGGCTACCGGCTGGTGGGA 6660  
Qy 6661 CACAGATGGGCATCTGTACCCGGCACCCCGAGGCTACCACTGTGGAGCAAGCATC 6720  
Db 6661 CACAGATGGGCATCTGTACCCGGCACCCCGAGGCTACCACTGTGGAGCAAGCATC 6720  
Qy 6721 CCTCTGTCAAGCTCTTTCCTGTGGCTTCTGAGGCCCAAGATGGATGGTGT 6780  
Db 6721 CCTCTGTCAAGCTCTTTCCTGTGGCTTCTGAGGCCCAAGATGGATGGTGT 6780  
Qy 6781 GGGAAAGATACAGTGGGAACCAAGGCGGTGACAGCTGCAAGTGAAGCTACACCTC 6840  
Db 6781 GGGAAAGATACAGTGGGAACCAAGGCGGTGACAGCTGCAAGTGAAGCTACACCTC 6840  
Qy 6841 CAGGAGGCGCTGAGGCACTGAGAGTGTCTGACACAGGCGTATGGAGCAACCGCAT 6900  
Db 6841 CAGGAGGCGCTGAGGCACTGAGAGTGTCTGACACAGGCGTATGGAGCAACCGCAT 6900  
Qy 6901 GTCCACCAACAGTGTCCCTGTGACTGTCTGATGTCAAGTACATCAGCGTGAAGCAT 6960  
Db 6901 GTCCACCAACAGTGTCCCTGTGACTGTCTGATGTCAAGTACATCAGCGTGAAGCAT 6960  
Qy 6961 GGGCGATGAGGCTTATCTTTGAGACACAGTATCAGTTCAGGCGCCAGCGTGAAGCAT 7020  
Db 6961 GGGCGATGAGGCTTATCTTTGAGACACAGTATCAGTTCAGGCGCCAGCGTGAAGCAT 7020  
Qy 7021 TGTGACCTGTGACTACTATACATGAGCAAGGGGTATCCGCTGTGAGGCAATGGGAA 7080  
Db 7021 TGTGACCTGTGACTACTATACATGAGCAAGGGGTATCCGCTGTGAGGCAATGGGAA 7080  
Qy 7081 TGGAGCCTGGGGACTCTAGGCCCACTGCGCATATCTCTGTGAGAGCTCCGAT 7140  
Db 7081 TGGAGCCTGGGGACTCTAGGCCCACTGCGCATATCTCTGTGAGAGCTCCGAT 7140  
Qy 7141 CCCCCCAATGGGCAACCGCATGGGACATCTGTCTACCGGGCAACAGCATCTTCTCC 7200  
Db 7141 CCCCCCAATGGGCAACCGCATGGGACATCTGTCTACCGGGCAACAGCATCTTCTCC 7200  
Qy 7201 TGGCAATTCGGGATACACTGTGGGCTCCAGGGGTGTGAGTGAATGGGCAATGGGCTC 7260  
Db 7201 TGGCAATTCGGGATACACTGTGGGCTCCAGGGGTGTGAGTGAATGGGCAATGGGCTC 7260  
Qy 7261 TGGAGTGGCTCTGAGTCCGCTGCTTGTGCTGACACTGTGGGACTCCTGAGCCCATTTGTC 7320  
Db 7261 TGGAGTGGCTCTGAGTCCGCTGCTTGTGCTGACACTGTGGGACTCCTGAGCCCATTTGTC 7320  
Qy 7321 AACGGAACATCAATGGGGAACTACAGCTACCGGGGAGTGTGTGACCAATGCAT 7380  
Db 7321 AACGGAACATCAATGGGGAACTACAGCTACCGGGGAGTGTGTGACCAATGCAT 7380  
Qy 7381 AACGGAACATCAATGGGGAACTACAGCTACCGGGGAGTGTGTGACCAATGCAT 7440  
Db 7381 AACGGAACATCAATGGGGAACTACAGCTACCGGGGAGTGTGTGACCAATGCAT 7440  
Qy 7441 GGGCAAGACCCCTTCTGTGTGCCAATTAACCTGTGACACCGAGCAACCTGTCAAGCGC 7500  
Db 7441 GGGCAAGACCCCTTCTGTGTGCCAATTAACCTGTGACACCGAGCAACCTGTCAAGCGC 7500  
Qy 7501 CTGACTCAGGGTAAACAGTTTAACTTCACGATGTGTCAAGTTTGTTCACACCTGTGG 7560  
Db 7501 CTGACTCAGGGTAAACAGTTTAACTTCACGATGTGTCAAGTTTGTTCACACCTGTGG 7560  
Qy 7561 TATATGGCTGAGGGGCTGTAGTCCCAATGCTGGGCAAGGGGCAATGGAATGACATG 7620  
Db 7561 TATATGGCTGAGGGGCTGTAGTCCCAATGCTGGGCAAGGGGCAATGGAATGACATG 7620  
Qy 7621 CTGCGCACTGAGAAATCAATCAATGATCTGTGACACCAAGAAATAGTGTTCGT 7680  
Db 7621 CTGCGCACTGAGAAATCAATCAATGATCTGTGACACCAAGAAATAGTGTTCGT 7680

Qy 7681 CAGGTCCAGCCAGGGGCGCGGACAGGTTCAAGTTGCGGACCACTGNGTCTTACCGGTGC 7740  
Db 7681 CAGGTCCAGCCAGGGGCGCGGACAGGTTCAAGTTGCGGACCACTGNGTCTTACCGGTGC 7740  
Qy 7741 AACCAAGGCTTCTACTCTGTGGGCAACCGAGTGTAGCTGACGAGGAGATGGACATGG 7800  
Db 7741 AACCAAGGCTTCTACTCTGTGGGCAACCGAGTGTAGCTGACGAGGAGATGGACATGG 7800  
Qy 7801 GACCGTCCCGGCCAGTGTCTCTTGTGTCTGTGGCCATCCGGGCTCCCGCTCAC 7860  
Db 7801 GACCGTCCCGGCCAGTGTCTCTTGTGTCTGTGGCCATCCGGGCTCCCGCTCAC 7860  
Qy 7861 TCCCAATGTCTGAGACAGTTATAGTGGGAGCATGTGGGATGGATACAGCTGCATCCG 7920  
Db 7861 TCCCAATGTCTGAGACAGTTATAGTGGGAGCATGTGGGATGGATACAGCTGCATCCG 7920  
Qy 7921 AAGCTACTCTGTGTGGGAAACAGCAACCGCATGTGTGGGCTGATGAGACATGGACTGGC 7980  
Db 7921 AAGCTACTCTGTGTGGGAAACAGCAACCGCATGTGTGGGCTGATGAGACATGGACTGGC 7980  
Qy 7981 TCCCTCTCTACTGTCTCAGGAAACAGCGTGGGAGTTGGGATGACCTGGGATCCGGCT 8040  
Db 7981 TCCCTCTCTACTGTCTCAGGAAACAGCGTGGGAGTTGGGATGACCTGGGATCCGGCT 8040  
Qy 8041 CATGGATCCGTTTGGGGGACAGCTTGTATCCAGGACATGTATGGGCTTCACTGTGAA 8100  
Db 8041 CATGGATCCGTTTGGGGGACAGCTTGTGTATCCAGGACATGTATGGGCTTCACTGTGAA 8100  
Qy 8101 GCTGSCACAGTGTCCGGGATGTGACAGCGCACTGTCAAGCCATGGCTGTGGAGC 8160  
Db 8101 GCTGSCACAGTGTCCGGGATGTGACAGCGCACTGTCAAGCCATGGCTGTGGAGC 8160  
Qy 8161 GGTGCGACCTGATGTGTGAGTATCTTGTGGGACCTGGGACTCCAGTAATGCC 8220  
Db 8161 GGTGCGACCTGATGTGTGAGTATCTTGTGGGACCTGGGACTCCAGTAATGCC 8220  
Qy 8221 CGAGTTGTGTGATGATAGGCGCTGTTTCTCCAGCTGTATGTATAGTGGCGGGAA 8280  
Db 8221 CGAGTTGTGTGATGATAGGCGCTGTTTCTCCAGCTGTATGTATAGTGGCGGGAA 8280  
Qy 8281 GGATATAGGCAACAGGCTGTCTCAGCGTCACTGTCTGGTCAATGGTATGGACAGGC 8340  
Db 8281 GGATATAGGCAACAGGCTGTCTCAGCGTCACTGTCTGGTCAATGGTATGGACAGGC 8340  
Qy 8341 AGTGACCTGAGTGTCTGTCTATTAACCTGTGTGACCTGGGATTCAGCCAAATGCCCTT 8400  
Db 8341 AGTGACCTGAGTGTCTGTCTATTAACCTGTGTGACCTGGGATTCAGCCAAATGCCCTT 8400  
Qy 8401 CGGCTGGGCAATGACTTCAAGTACAAACCTGTGACATATCAATGTGTCTGTGCTAT 8460  
Db 8401 CGGCTGGGCAATGACTTCAAGTACAAACCTGTGACATATCAATGTGTCTGTGCTAT 8460  
Qy 8461 ATGATGAGTACATAGAGTATCTGTGAGCTGACCAAGGACCGGACATGGAATGGA 8520  
Db 8461 ATGATGAGTACATAGAGTATCTGTGAGCTGACCAAGGACCGGACATGGAATGGA 8520  
Qy 8521 ACCAAGCCCGTGTGCAAGCTCTCATGTGCAACCACTCCGCTCATGCCAAATGGGAAG 8580  
Db 8521 ACCAAGCCCGTGTGCAAGCTCTCATGTGCAACCACTCCGCTCATGCCAAATGGGAAG 8580  
Qy 8581 GTGGTGGGCTGTGACTTCAATGTGGGCTCAAGTGTACTTATGCTGTGAGGGGTAC 8640  
Db 8581 GTGGTGGGCTGTGACTTCAATGTGGGCTCAAGTGTACTTATGCTGTGAGGGGTAC 8640  
Qy 8641 CAGCTCTCCCTGCGCGGATGTTCACCTGTGAGGAGAAATGGGCTCTGACCGGAGAGCTG 8700  
Db 8641 CAGCTCTCCCTGCGCGGATGTTCACCTGTGAGGAGAAATGGGCTCTGACCGGAGAGCTG 8700  
Qy 8701 CCTCAGTGTTCCTGTGTCTGTGGGATCTGTGTCTCCGTCCGTGGAGAGAGAG 8760  
Db 8701 CCTCAGTGTTCCTGTGTCTGTGGGATCTGTGTCTCCGTCCGTGGAGAGAGAG 8760



Db	241	GAAAGGGGCAAAAGACTAGGCTCGGATTTCAAGTTAGGATCCAGGCTCACTTCACTTGC	300
Qy	301	AACGAGGGCTATGACCTTGCAAGGGTCCAAAGCGGATCACCTGTATGAAAGTGAAGCATG	360
Db	301	AACGAGGGCTATGACCTTGCAAGGGTCCAAAGCGGATCACCTGTATGAAAGTGAAGCATG	360
Qy	361	TTTGGCGGCTTGAGAGCAACAAGGCAAGTCTGCGAGCGCCGATGTGTGATGCCACCTT	420
Db	361	TTTGGCGGCTTGAGAGCAACAAGGCAAGTCTGCGAGCGCCGATGTGTGATGCCACCTT	420
Qy	421	CGAGGCGCCCTGGGGCATCATCACTGCCCAATTTCCCATTCAGTATGACAACATGCA	480
Db	421	CGAGGCGCCCTGGGGCATCATCACTGCCCAATTTCCCATTCAGTATGACAACATGCA	480
Qy	481	CACGTGTGTGGATCATCAGACACTCAACCCCTCCAAAGTGTATCAAGCTCGCTTTGAG	540
Db	481	CACGTGTGTGGATCATCAGACACTCAACCCCTCCAAAGTGTATCAAGCTCGCTTTGAG	540
Qy	541	GAGTTTGATTTTGGAGAGGGGCTATGACACCTTGACGCTGGTGTATGTTGTGATGAG	600
Db	541	GAGTTTGATTTTGGAGAGGGGCTATGACACCTTGACGCTGGTGTATGTTGTGATGAG	600
Qy	601	GACCAAGAAAGATGTTCTCTACATGTCTCAAAATGCTGCAATGACAGCCCTCACACCCA	660
Db	601	GACCAAGAAAGATGTTCTCTACATGTCTCAAAATGCTGCAATGACAGCCCTCACACCCA	660
Qy	661	GGCTCTCGCATCCCAAGAGAGCATGTCTGGGACATCTTGAAGGCAGAAATGATCTGTACTT	720
Db	661	GGCTCTCGCATCCCAAGAGAGCATGTCTGGGACATCTTGAAGGCAGAAATGATCTGTACTT	720
Qy	721	GAGATCTGTGCTGACATTAGAGATTCAAGATCAAAGTCAAGTTCAGTAGAGGAATCTCCA	780
Db	721	GAGATCTGTGCTGACATTAGAGATTCAAGATCAAAGTCAAGTTCAGTAGAGGAATCTCCA	780
Qy	781	AAGATCTTATATGCTGTGGAACTTGTGCTCTTGGGACAGATTCGACAGGGGCAATTCG	840
Db	781	AAGATCTTATATGCTGTGGAACTTGTGCTCTTGGGACAGATTCGACAGGGGCAATTCG	840
Qy	841	GGTACACCTTGACATACCTGCATATGAGCGGAGGGAAAGGCTCCCGATTTACACAGGTGAC	900
Db	841	GGTACACCTTGACATACCTGCATATGAGCGGAGGGAAAGGCTCCCGATTTACACAGGTGAC	900
Qy	901	ACACTCAAAGTTTGAAGTGCACAGCGGCTTTAGCGTGGTGGGACAGAAAGCAATCAATGC	960
Db	901	ACACTCAAAGTTTGAAGTGCACAGCGGCTTTAGCGTGGTGGGACAGAAAGCAATCAATGC	960
Qy	961	CAAAAGAAATACCAATGTCGGCTTACAGGCGAGCTGCGTTCCTCGCTTCTTCAAC	1020
Db	961	CAAAAGAAATACCAATGTCGGCTTACAGGCGAGCTGCGTTCCTCGCTTCTTCAAC	1020
Qy	1021	TTTCAACAGCGGCTGCGGGTTGTCTGTCTCCCAATCACCAAGAGGACTATGGAACACAC	1080
Db	1021	TTTCAACAGCGGCTGCGGGTTGTCTGTCTCCCAATCACCAAGAGGACTATGGAACACAC	1080
Qy	1081	CTTCACTGTGTCTGGCTCATCTTGGCCAGGCTGAGAGCCGCATTCACCTTGCTTCAAC	1140
Db	1081	CTTCACTGTGTCTGGCTCATCTTGGCCAGGCTGAGAGCCGCATTCACCTTGCTTCAAC	1140
Qy	1141	GACATTTGAGTGAAGCTCAAGTTGATTTCTGTGTCATCAAGATGAGGCGCACCGCGAG	1200
Db	1141	GACATTTGAGTGAAGCTCAAGTTGATTTCTGTGTCATCAAGATGAGGCGCACCGCGAG	1200
Qy	1201	GGGCGCGGCTCGGGGACCTTCTCAAGGAAACAAGTCCCTCTCAATCAACAAGAGTGGC	1260
Db	1201	GGGCGCGGCTCGGGGACCTTCTCAAGGAAACAAGTCCCTCTCAATCAACAAGAGTGGC	1260
Qy	1261	CACGTGCGCGTCTCGAGTTCCAGACTGACCACTTCCACAGGGAAGAGGGGCTTCAATCTC	1320
Db	1261	CACGTGCGCGTCTCGAGTTCCAGACTGACCACTTCCACAGGGAAGAGGGGCTTCAATCTC	1320
Qy	1321	ACTTTTACCACTTTCGACACACGAGTCCCGGATCTTGCGTTCCAGTAAATGCGAA	1380

Db	1321	ACTTTTACACACTTTCGACACAAAGAGTGGCCCGGATCTCTGGCCCTTCCAGTAAATGGCAAA	1391
Qy	1381	CGTTTGTGGGGACAGCCTTCCAGCTGGGCAAGCTCCATCTTCCTCTGTGATGAAGCTTC	1440
Db	1381	CGGTTTGGGGACAGCCTTCCAGCTGGGCAAGCTCCATCTTCCTCTGTGATGAAGGCGCTTC	1440
Qy	1441	CTTGAGGACTGAGGGGCTCAGAGACCATACATCGTGGCGCTCTGAAAGAGGGCAGCGTGGCTGG	1500
Db	1441	CTTGAGGACTGAGGGGCTCAGAGACCATACATCGTGGCGCTCTGAAAGAGGGCAGCGTGGCTGG	1500
Qy	1501	AACAGCGCTGTGCTGCGGGTGTGAAGCTCCCTGTGGTGGTCACTCGACTTCGGCCAGCGGC	1560
Db	1501	AACAGCGCTGTGCTGCGGGTGTGAAGCTCCCTGTGGTGGTCACTCGACTTCGGCCAGCGGC	1560
Qy	1561	ACCATCTCTCTCCGGGCTGGGCTGGCTGGCTTTCACAGAGATGGCTTGAAGCTGTGCTGGGTG	1620
Db	1561	ACCATCTCTCTCCGGGCTGGGCTGGCTGGCTTTCACAGAGATGGCTTGAAGCTGTGCTGGGTG	1620
Qy	1621	ATTGAGGCCCAAGCCAGGCTACCCCATCAAATATCACTTTCGACAGATTCAAAACCGAAGTC	1680
Db	1621	ATTGAGGCCCAAGCCAGGCTACCCCATCAAATATCACTTTCGACAGATTCAAAACCGAAGTC	1680
Qy	1681	AACATATGACACCTCGGGAAGTACGGGATGGGGGCGACTTAATCAGGGCCCTGATGGGGTT	1740
Db	1681	AACATATGACACCTCGGGAAGTACGGGATGGGGGCGACTTAATCAGGGCCCTGATGGGGTT	1740
Qy	1741	TACCACGGGAACCAAGTTCGCCAGTTCCCTCATCGACACACAGCACTACCTTCACTCTC	1800
Db	1741	TACCACGGGAACCAAGTTCGCCAGTTCCCTCATCGACACACAGCACTACCTTCACTCTC	1800
Qy	1801	TTCTCTACCGACAGAGAGTCACTCGGACATGGGCTTCCAGCTCCGCTATGAGACTATTAACA	1860
Db	1801	TTCTCTACCGACAGAGAGTCACTCGGACATGGGCTTCCAGCTCCGCTATGAGACTATTAACA	1860
Qy	1861	CTGAGAGTCAGACCACTGTGGAATCCAGGAATCCCACTAAATGGACAGCGTCATGGGAAT	1920
Db	1861	CTGAGAGTCAGACCACTGTGGAATCCAGGAATCCCACTAAATGGACAGCGTCATGGGAAT	1920
Qy	1921	GACTTCTACGAGGGGCGGCTGGTGAACCTTCAGCTGTGACTCGGGCTACACATTAAGTGAC	1980
Db	1921	GACTTCTACGAGGGGCGGCTGGTGAACCTTCAGCTGTGACTCGGGCTACACATTAAGTGAC	1980
Qy	1981	GGGAGGCTCTGAGGTGAGCCCACTTCAGGTGAGCCGGGCGCTGGCCAGTGTGAA	2040
Db	1981	GGGAGGCTCTGAGGTGAGCCCACTTCAGGTGAGCCGGGCGCTGGCCAGTGTGAA	2040
Qy	2041	GCTCTGTGTGGTGGCTTCAATTCAAGGCTCCAGTGGGACATCTTGTGGCAGGGTTCCT	2100
Db	2041	GCTCTGTGTGGTGGCTTCAATTCAAGGCTCCAGTGGGACATCTTGTGTGGCAGGGTTCCT	2100
Qy	2101	GACTTCTACCCCAACAATTGGAATGGAACCTGATATGCAATGGAAGGAT	2160
Db	2101	GACTTCTACCCCAACAATTGGAATGGAACCTGATATGCAATGGAAGGAT	2160
Qy	2161	GTGTTCCTTCACTTTCACACCTTTCACACCTTTCACACCTTTCACACCTTTCATCACT	2220
Db	2161	GTGTTCCTTCACTTTCACACCTTTCACACCTTTCACACCTTTCACACCTTTCATCACT	2220
Qy	2221	GAGAAACGGACGCTTCAACCCAGCCCTGAGGCACTTAATGGAATTCGGGCTGCCAGCTCCC	2280
Db	2221	GAGAAACGGACGCTTCAACCCAGCCCTGAGGCACTTAATGGAATTCGGGCTGCCAGCTCCC	2280
Qy	2281	ATCAGCGCTGGGGCTCTATGAGCACTTACATGACCCAGGTCGGCTCATCTGTGAATTTCTCC	2340
Db	2281	ATCAGCGCTGGGGCTCTATGAGCACTTACATGACCCAGGTCGGCTCATCTGTGAATTTCTCC	2340
Qy	2341	ATGTCTATATGAAGATTCAAATCATCACTTCTCAGAGTACGACTTGAAGCCCTGTGAGAG	2400
Db	2341	ATGTCTATATGAAGATTCAAATCATCACTTCTCAGAGTACGACTTGAAGCCCTGTGAGAG	2400
Qy	2401	CCCGAGGCTCCAGCTTACAGATCCGGAAGGGCTTCGAGTTTGGCTGTGGCGACACTTGG	2460
Db	2401	CCCGAGGCTCCAGCTTACAGATCCGGAAGGGCTTCGAGTTTGGCTGTGGCGACACTTGG	2460

[illegible]

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Db	3641	GAGATCAGCTGTGTGAAGATCCGAAACAGGTTCTTTGTGGACAGCCAGCCGCGCAATATGC	3600
QY	3601	ATGCGTCCCTCGCGGGGAGAACCTCGACAGGACCATCTGGAGTGCATCTCTGCACCAATTAC	3660
Db	3601	ATGCGTCCCTCGCGGGGAGAACCTCGACAGGACCATCTGGAGTGCATCTCTGCACCAATTAC	3660
QY	3661	CCGAAACCTTACCCCGCAGGCAAGAGTGTGACTGAAAGTACCGTCTCCACAGACTAC	3720
Db	3661	CCGAAACCTTACCCCGCAGGCAAGAGTGTGACTGAAAGTACCGTCTCCACAGACTAC	3720
QY	3721	GTATCGCCCTGGTATTTTAACTCTTTAACCGGAGCGCTGGCTGTAGCTTCCTCCATATC	3780
Db	3721	GTATCGCCCTGGTATTTTAACTCTTTAACCGGAGCGCTGGCTGTAGCTTCCTCCATATC	3780
QY	3781	TACGACGAGCGGAGCTTCTTCAGCCCTCTCAAGGAAGCTTCTATGAGCTCCAGCTCCCA	3840
Db	3781	TACGACGAGCGGAGCTTCTTCAGCCCTCTCAAGGAAGCTTCTATGAGCTCCAGCTCCCA	3840
QY	3841	GCGCGGATTTGAAGAGAGAGCAACAGCTCTTCTTCGCTTCGCAAGCATGATCTGTG	3900
Db	3841	GCGCGGATTTGAAGAGAGCAACAGCTCTTCTTCGCTTCGCAAGCATGATCTGTG	3900
QY	3901	AGCAATGCTGCGCTTGTGATTTGACTATTCAGAAAACCGCGGAGTCAATGTTTGAATCCT	3960
Db	3901	AGCAATGCTGCGCTTGTGATTTGACTATTCAGAAAACCGCGGAGTCAATGTTTGAATCCT	3960
QY	3961	GGTTTCATCAAGAAAGGACACACGGGTGGGTCCGACTTGAAGCTGGGCTCTCCGTACCC	4020
Db	3961	GGTTTCATCAAGAAAGGACACACGGGTGGGTCCGACTTGAAGCTGGGCTCTCCGTACCC	4020
QY	4021	TACTACTGCGACGGGGGCTACGAAAGTTGAGGGACCTCGAACCTGAGTGCATCTCGGGG	4080
Db	4021	TACTACTGCGACGGGGGCTACGAAAGTTGAGGGACCTCGAACCTGAGTGCATCTCGGGG	4080
QY	4081	CCTGATGGGAAAGCCCGTGTGGAAACAATCCCGGCACTTGCACAGCCCGCTGTGGGGGA	4140
Db	4081	CCTGATGGGAAAGCCCGTGTGGAAACAATCCCGGCACTTGCACAGCCCGCTGTGGGGGA	4140
QY	4141	CAGTATGGGGGTTGCGACGAGAGTGTGTTTCCGCCCACTAACCCCGCAAGAACTACACCAAT	4200
Db	4141	CAGTATGGGGGTTGCGACGAGAGTGTGTTTCCGCCCACTAACCCCGCAAGAACTACACCAAT	4200
QY	4201	GGAACAGATCTGCTGTATTTTGTGTTACTGTGCCAAGGACTATGTGTGTTTGGCAGTTTC	4260
Db	4201	GGAACAGATCTGCTGTATTTTGTGTTACTGTGCCAAGGACTATGTGTGTTTGGCAGTTTC	4260
QY	4261	GCGTCTTTTTCACAGGGGCTCCACACGACGTGTGGAAGTTTCAGACGGGCAACAGCCAGCAC	4320
Db	4261	GCGTCTTTTTCACAGGGGCTCCACACGACGTGTGGAAGTTTCAGACGGGCAACAGCCAGCAC	4320
QY	4321	TGCGGGCTCTCAGACTCCCTCTCGGGCTCCCATACAGAGAACTCATGCTCTTGGCGACC	4380
Db	4321	TGCGGGCTCTCAGACTCCCTCTCGGGCTCCCATACAGAGAACTCATGCTCTTGGCGACC	4380
QY	4381	TCCATACAAATTTCTCATTTAAGTTCAAGCGCAAAAGGCTCTGCACACAGCCAGAGGCTTTCAC	4440
Db	4381	TCCATACAAATTTCTCATTTAAGTTCAAGCGCAAAAGGCTCTGCACACAGCCAGAGGCTTTCAC	4440
QY	4441	TTTGTCTACCAAGCGGTTCTCGAACACAGCGCAACGAGTGAAGCTGTGCGCGGAACCC	4500
Db	4441	TTTGTCTACCAAGCGGTTCTCGAACACAGCGCAACGAGTGAAGCTGTGCGCGGAACCC	4500
QY	4501	CGCTATGGCAAGAGGCTGGGCACTGACTTCTCGGTGGGGGCATGTGCGGTTGGAATGC	4560
Db	4501	CGCTATGGCAAGAGGCTGGGCACTGACTTCTCGGTGGGGGCATGTGCGGTTGGAATGC	4560
QY	4561	AACCTCGGCGTAATCCCTGACGGGGTCCGCAAGATTCGAGTGCCTCTGTGCTGGGGCC	4620
Db	4561	AACCTCGGCGTAATCCCTGACGGGGTCCGCAAGATTCGAGTGCCTCTGTGCTGGGGCC	4620
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Query Match      26.8%; Score 2715.4; DB 15; Length 7323;
Best Local Similarity 66.8%; Pred. No. 0;
Matches 3952; Conservative 0; Mismatches 1879; Indels 84; Gaps 3;

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DB 1128 GGAAGCATTAAAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1187
QY 223 CCAGACCTGTGCAATCCGAAAGGCGAAAGACTAGGCTCGGATTTCAAGTTAGAGATCC 282
DB 1188 CCGAGATCTGGGATTCAGAAAATGATGAGAGAGAGGTTCCGACTTCAAGGTTGTGTGA 1247
QY 283 AGGTCAGATTCACCTGCAACGAGGCTATGACCTGCAAGGTTCCAGGCGATCACTGT 342
DB 1248 AATGTCAATTTTCAATGTAGAGCAATTAAGTCTTCAGAGGATCTAAAGCATCACTGT 1307
QY 343 ATGAAAGTGAAGCAATGTTTTCGAGCTGAGAGCAACAGAGCCAGTCTGCGAGAGCCGC 402
DB 1308 CAGAGAGTTAAGAGAGCGCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1367
QY 403 ATGTGTGATGCCCACTTTGAGAGCCCTTGGGCAATCATCACTCCCAATTTCCCAT 462
DB 1368 AATGTGTGATCCCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1427
QY 463 CAGTATGACAAATGACACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 522
DB 1428 CAGTATGACAAATGACACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1487
QY 523 ATCAAGCTGCTTTTGAAGAGTTTGAATTTGAAGAGGCTATGACACCTTGAAGGCTGCT 582
DB 1488 ATCAAGCTGCTTTTGAAGAGTTTGAAGAGGCTATGACACCTTGAAGGCTGCTGCT 1547
QY 583 GATGTGTGTGAGAGTGGGAGCCAGAGACAGTTCTCTCATGTCTCAAAATGCTGCACT 642
DB 1548 GATGTGTGTGAGAGTGGGAGCCAGAGACAGTTCTCTCATGTCTCAAAATGCTGCACT 1589
QY 643 GACAGCCTTCACACCCAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 702
DB 1590 -----CTCAGCGGATTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1634
QY 703 CAGAAATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 762

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DB 1635 CAGATGTGCTTCAATCTGCAATGCGATATAGCAATTCGCTCACTGGGT----- 1683
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DB 1684 -----TTAAAGCTGTTCACAAAGA 1703
QY 823 ATCGAGCAGAGGAGTGGGCTGACCTTGTGATCTTGTGATATGCGGAGGAGAGGCTCC 882
DB 1704 ATTTGAAAAGGAGGTTGGGAGTCTGTGAATCCCGGCTTATGGAAGCGGAGCGAGC 1763
QY 883 CGGTTTCAACGCGTGAACACTCAAGTTTGAAGTGGCCAGCCGCTTTGAGCTGTGTGGA 942
DB 1764 AGTTCTTCCATGAGGATTCATTAATGCTTGAATGCTTGTGAGCTGTGTGAGCTGTG 1823
QY 943 CAGAAAGCAATTCATGCTCCAAAGATTAACCAATGTGTGTGTGTGTGTGTGTGTGTGTGT 1002
DB 1824 GAGAGAGTTATACCTGTGACAGCAACCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1883
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DB 1884 TTTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1943
QY 1063 GAGACTATGAGCAACACTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1122
DB 1944 GAGGAATATGGAACCAATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2003
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DB 2004 ATTCACCTTATCTTAAATGATTTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2063
QY 1183 GATGGGCGCAACCGCGAGGCGCCGCTGTGGGACCTTCAAGAAACAGCTTCCCTCC 1242
DB 2064 GATGATGGAATTTGTGACATTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2123
QY 1243 TCCTATCAACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1302
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DB 2184 GCGAGAGGTTTAAATCACTTAAACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2243
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QY 1483 GAGGCGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1542
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DB 2544 AGATTCAAAACGAGGTCAATATGACACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2603
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DB 2604 TCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2663
QY 1783 AACTACTTCACTCTCTTCTTCAACGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1842
DB 2664 AACTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2723

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OY	1813	UGCTATGAGACTTATTAACCTGCACTGACAGAACCAACTGTCTGGATTCAGAGAAATCCCACTAAAT	1902
Db	2724	CACATATGAGAAATGTGACCGCTTGAGTCGGAAATTCCTGGCTGGAGACCGGGGATCCCTGTGAAC	2783
OY	1903	GGACAGCCTCAATGGGAATGACTTTCACCTGGGCGCGCTGGAGACCTTCAGCTGTGACTCG	1962
Db	2784	GGCCATCGCCACGGGTGAGACTTTGGGATCAAGTGTCAACATGTACTTTTCAGCTGTGACCCG	2843
OY	1963	GGCTACACATTAAATGATCGGGGAGCTCTTGAGTGTGAGCCCACTTTCAGTGAACCCG	2022
Db	2844	GGGTACACACTAAAGTACGACGAGCGCCCTCGCTGTGTGAGAGAAACCAACAAATGGAACAC	2903
OY	2023	GGCCGGCCCAATGTGGAAGCTCTGTGTGTGGCTCAATCAAGGCTCCAGGTGGAGCAATC	2082
Db	2904	GCCTTGCCCACTGCGACGCTCTTATGTGAGGCTATCAAGGAAAGTGGAAACAGTC	2963
OY	2083	TTGTGCGCAGGAGTTCCTGACTTTCACCCCAACATTGAACTGCACTGTGATTATGAA	2142
Db	2964	CTTTCTCTGGGTTTCAGATTTTATTCAAACTCTTAACTGTGACGTGACCATTTGAA	3023
OY	2143	ACATTTCAATGGCAGGGGTGTGTTCTTCACTTTCCACACTTCCACTGTGAAAGTGGCAT	2202
Db	3024	GTGTCTCATGGGAAAGGAGTTCAAAATGATCTTTTCAACACTTTCATCTTGAAGATTCAC	3083
OY	2203	GACTACCTCTCATCTACTAGAGAACGGCAGCTTCAACCCAGCCCTGAGGACGTAATCTGA	2262
Db	3084	GACTATTTACTGATACAGAGAGATGGAAGTTTTTCCAGGCCCGTTGCCAGGCTCACCGGG	3143
OY	2263	TCTCGGCTGCGAGCTCCCATCAGCGGCTGGGCTTATGGCAACTTCACTGCTCCAGGTCGC	2322
Db	3144	TCGGTGTTCCTCATACAGTCAAGGCAAGGCGCTGTGGAAACTTCACTGACCCACATTCGG	3203
OY	2323	TTCACTCTGTGATTTCTCATGTCATATGAAGAATTCAACATCACTTCTAGAGTAAGAC	2382
Db	3204	TTTATATAGACTTTCATATTTCTGTACAGAGGCTTCAATATCAATTTTTCGAAATATGAC	3263
OY	2383	TTGAGCCCTGTGAGAGAGCCGAGGTCTCCAGCTTACAGCATCCGAAAGGCTTGACGTTT	2442
Db	3264	CTGGAGCATGTGATGATCTGTGAGATCCCTGCTTCACGCGAAGATGTGTTTCACTTT	3323
OY	2443	GGCGTGGGCGACACTTGAACCTCTCTCTGTCTTCCCGGGTACCGCTGTGAGAGGCAACGCGC	2502
Db	3324	GGTGTGGGAGACTCTGTACGTTTCTGTCTTCTGTGGATATCGTTTGAAGAGGTGCCACC	3383
OY	2503	CGCATCAAGTGCCTGGGGGGGAGACGGCGCTGTGAGACTGCGCTCTGCCAAGGTGTGTT	2562
Db	3384	AAGCTTACTCTGTGGGTGTGGGGCGCGCTGTGTGGAATGCACTCTGTGCCAAGGTGTGTG	3443
OY	2563	GCTGAGTGTGGGAATTCAGTCAAGGCACTCAAGGTACTTTGTCTGTCTCCCAACTTTCT	2622
Db	3444	GCCGGAATGTGGAGCAAGTGTCAAGAGGAATGAGGAACATTACGTCTCCAAATTTTCCA	3503
OY	2623	GTGAACCTCAATTAACAATCAGAAATGCACTTACTCACTCCAGACCCAGCGGAGAGGGA	2682
Db	3504	TTCAAATTATGATTAATCACTAGAGTGTATCTATAAATATAGAAACGAAGCGGCAAGGCG	3563
OY	2683	ATTCACTGAAAGCCAGGGCAATTGCMACTCTCCGAAAGAGATGTCTTCAAGTTTATGAT	2742
Db	3564	ATCCACTTTAGAACAGAAAGCTTCAGCTGTTTGAAAGAGATCTTAAAGTATATGAT	3623
OY	2743	GGCAACAACTCCGCCCTTTGTGTGGAGTTTTTAAAGCAATCTTGAGATGATGGGGGTG	2802
Db	3624	GGAAAGACAGTTCTCTCAAGTCACTGAGGCAAGTTCATTAAGAAATCTTGGGGGTG	3683
OY	2803	ACTTTGAACAGCACTCCAGCAAGTGTGGCTGTGATTTTCACTCACTGATCTGAAAAACAC	2862
Db	3684	ATCTCAAAACAGCACTCAATCACTGTGTGAGTTCAACACCAATGATCTGACAC	3743
OY	2863	AGCAAGGCTTTGAATGCACTTTTTCAGCTTTGAATCTCAATGATGAGAACCCGGA	2922
Db	3744	GACCAAGGTTTTCACCTCACTATACAGTTTGTATCTGTATAATATGAGAGATCCGGGC	3803

QY	2923	ACCCCAAGTTTGGCTACAAAGTTCAATGATGAAGTCAATTTTGCAGGAGACTCCGTGC	2982
Db	3804	ATCCCTTAATCTACGGCTAATAGATCCGTATATAAGGCCACTTACCGACATGTAGTCTG	3863
QY	2983	TTCAAGCTGTACCTCGAATACAGCTCGGGGGTATGTAGAGCATGTCTGTCTGATGTGA	3042
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QY	3103	AGAGGAGAGGTGTGGGGCAGGTGTGTACCCGGGTATCCAGTCTCCCTATGAACAATAT	3162
Db	3984	CATGACAGCCACATCAGGACGAATATGTGCTCCCTGGCTATCCAGCTCCGTAAGACAACAC	4043
QY	3163	CTCAACATCATCTGGACCATGGAAGACAGAGGCCGGGTGTCACTATGGGCTACATTTCTGT	3222
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Db	4104	GTTTTTCGACAGAGAGATGTGCTCAAGACATCTCAAGGTCTGTGGAGCGGGCCGGTGTGACGT	4163
QY	3283	GGGGTTCGTGTGAAGAGCTGATGTGTCCGGCCCTCCGCCAAGACCTGTGATACACTTC	3342
Db	4164	GACATCTCTGTGAAGAGATGTGTGCTCCGCCCTTCCGAGAGCATTCACAGCACCTTC	4223
QY	3343	AACTCGGTGTCTGTGAGTTGAGCATGTGACTTTCTTCAACACAGACAGGGCTTTGGCATTT	3402
Db	4224	AACTACTACCTCTGCAATTTGACAGGCACATTTCTTCAACACAGTCTGTGCTTCTTCATTC	4283
QY	3403	CAATTTTCAGTGTCCACAGCAACGTCTGTCAATGACCTGTGGATCCGCAAGATGTGAGT	3462
Db	4284	CAGTTTCTCACTCAATTTGACAGCCACTGTATACGATTCAGGTATGTGCCAATAATGTGACAC	4343
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Db	4404	CAGCTCCAAGACAAAGCCAAATATCCTGTGTGACGTGAATTAACCCGTTCTTTTGGCAA	4463
QY	3583	CCGAGCCCGCAACATGTATGCTTCCCTCGCGGGGAGACTGTGACAGGACCACTGTGAGTTC	3642
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QY	3643	ATCTCTTGCAAAATTACCCAGAACCCCTTACCCGCAAGGACGAGTGTGACTGGAAGTGTG	3702
Db	4524	ATTTTGTACCCCACTACCCACAGCCGTAATCTCTGTGGAGGAATGTGACTGGAAGTGA	4583
QY	3703	ACCGTCTACACGACTACGTATGTGCTTGTATTTAACTTTAACTTTAACTTTGAAGCTGTGC	3762
Db	4584	AAAGTGAACCCGGACTTGTGTATGTGCTTGTATTTCAAAAGTTTCAACATGAGACCCAGC	4643
QY	3763	TATGACTTCTTCAATCTATACGAGGAGACTCTCAGCCCTCTCATATGAGAACTTCTC	3822
Db	4644	TATGACTTCTTACATCTTATGAAAGGGAATTTTCAACAGCCCCCTCATTTGGAGTTTAC	4703
QY	3823	TATGTCTCCCAAGCTCCAGGCCGATTTGAAAGACAGACAGCAAGCTTCTCGCTTC	3882
Db	4704	CAGGCTCTCAAGGCCCCAGAAAGATTAAGATGTAGCGGAAACAGCTGTCTTCTGGCAATTT	4763
QY	3883	CGCAGCGATGCATCTGTGACGAATGTGTGCTTCTGTCAATGACTATACGAAATCCCGGG	3942
Db	4764	CGAGTGTATGTCTCTGTGTGGCTTTTCAAGGTTGCCATTTGAATTTTAAAGAAACCAAGG	4823
QY	3943	GAGTCAATTTTGAATCTGTTCATCAAGAAACGACACAGGTTGTGGGTCCGACTGTGAAG	4002
Db	4824	GAACTTGTTTTGAACCCAGAAATTTAATGAATGTGACACAGAGTTTGAACACGACTTCAG	4883
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FILE REFERENCE: 9052-144
CURRENT APPLICATION NUMBER: US/10/276,934
CURRENT FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: PCT/GB01/02240
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: GB0012186.3
PRIOR FILING DATE: 2000-05-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
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US-10-276-934-6
Query Match      26.8%; Score 2715.4; DB 15; Length 8034;
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Matches 3955; Conservative 0; Mismatches 1879; Indels 84; Gaps 3;
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Db      1778 CAAGTGAAGAAAGGAGATTGAGTGAAGTCAAGAGAGATGATGCTGCCAGCAAGAT 1837
QY      163 AACAGCCAGAGAGCTGTGTCTTAACTACAGTGTGTGTCCAGAGCAATATATGTGT 222
Db      1838 GGAAGGCATTAATACTGTCTTGAAGCCAGAGAGTGTGATTTGCTCTGACATGTGT 1897
QY      223 CCAAGACCTGGCATACCCGAAAGGGGCAAGACTAGAGTTCGAGTTTCAAGTTAGATCC 282

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Db      1898 CCAAGATCTGGGATTCAGAAAAATGTGTAAGAGCAGAGTTCCGACTTCAAGGTTGTGCA 1957
QY      283 AGCGTCAAGTTCACCTGCAAGAGGCGTATGACCTGCAAGGGGTCAGAGGATCACTGT 342
Db      1958 AATGATCACTTTTCATGTAGAGCAATTAAGTCTCAGAGGATCTTAAGACATCACTGT 2017
QY      343 ATGAAGTGAAGCAATGTTTTCGCGCTGAGAGCAGACAGGCGAGTGTGCGAGCCCG 402
Db      2018 CAGAGGTTACAGAGAGCTGCTGCTTGAAGTACAGAGGCCCATCTGCCAGAGGAA 2077
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QY      1063 GAGGATATGAGGAAACACCTCCATGTCGTGCTCATCTGCGCAGAGCCCTGAGAGCGCG 1122
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Db      2714 ATTCACCTATATCTTAAATGATTTTGAATGTTGAGCTCAATTTGATCTCGGGTCAAG 2773
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DB 4034 GGTGTGGAGACTCTCTGACGTTTCTGTGCTTCCGGAATTCGTTTGAAGTGTCCAC 4093  
QY 2503 GGCATCAGCTGCTGGGGGGGAGAGCGGCTGTGTGAGCTGCTTCTCCAGAGTGTGT 2562  
DB 4094 AAGCTTACCTGCTGGGGGGGCGCGTGTGTGAGTGAACCTTCCAGAGTGTGTG 4153  
QY 2563 GCTGAGTGTGGAATTCAGTCAAGGCACTCAGGCTATTGTGTGTCTTCCCACTTCTCT 2622  
DB 4154 GCCGAATGTGAGCAAGTGTCAAGGAATGAGGAACATTACTGTCTCCAAATTTTCA 4213  
QY 2623 GTGAATCAATTAATCAATGATGATCTTATCTCATCCAGACCCAGCCAGGAGGGA 2682  
DB 4214 TCCAAATTAATTAATCAATGATGATCTTATTAATAAGAAAGAAAGCCGCGAGGCG 4273  
QY 2683 ATTCACTGAAAGCCAGGAGCTTGAACCTCCGAGAGAGTGTCTCAAGTTTATGAT 2742  
DB 4274 ATCCACTTGAACACGAGCTTCCAGCTTGTGAAGAGATCTTAAGATTAATGAT 4333  
QY 2743 GCGAACAACTCCGCGCTTGTGTGTGAGTTTGTAGCCATTCTGATGATGAGGAGTGT 2802  
DB 4334 GGAAGAGCACTTCTCAGCTGCACTGAGGACGTTCACTAAATGAACTTCTGGGCTG 4393  
QY 2803 ACTTGAACAGACATCCAGAGTCTGTGCTTATTTATCACTGATGCTGAAACACC 2862  
DB 4394 ATCTTAACAGACATCCATCACTGCTGTGATGATGATGATGATGATGATGATGAT 4453  
QY 2863 AGCAAGGCTTGTGAATGACATTTTCCAGCTTGAATCAATGAATGAGAGCCAGGA 2922  
DB 4454 GACCAAGTTTTCACACTCACTATACAGATTTGATGTGTAATGTGAGATCCCGG 4513  
QY 2923 ACCCCCAAGTTTGGCTTCAAGAGTTTCAATGATGAGAGTATTTTGAAGGAGCTCGTGTCC 2982  
DB 4514 ATCCCTAATCAAGCTTATGAGATCCGATGAGGAGCCATTTACCACTGATGATGAT 4573  
QY 2983 TTCACTGTGACCTGTGATCAGCTGTGGGGTATGATGAGAGCTGTGTGTGTGATGGA 3042  
DB 4574 TACAGTTGCAACCTGGGGTATGCGATGATGAGCAACCCCTGACCTTGTGTGAGTGA 4633  
QY 3043 GAGGCGCGACCTTGGGACCGGCTTGTCCACCTGTGTGCGCAGAGTGTGAGGAGCAGTG 3102  
DB 4634 GACAGAGAGTGTGGGACCAACCATCACTTCTGTGATGAGGAGATGTGTGTGATG 4693  
QY 3103 AGAGGAGAGTGTGGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3162  
DB 4694 CATGACCCATCAAGACCAATATTTGTCTCCGCTATCCAGCTCCGATGACCAAC 4753  
QY 3163 CTCAACTGACCTGTGACATCAAGAGAGGCGGCTGACCATTTGGGCTTACCTCTCG 3222  
DB 4754 CTCACCTGACCTGTGATTAAGAGGACAGCCAGGAAGCATTTAGCTTCCATTTCAAT 4813  
QY 3223 GTGTGTGACAGAGAGGTTTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3282  
DB 4814 GTTTGCAACAGGAGATGT 4873  
QY 3283 GGGGTTCTGTGAAGAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3342  
DB 4874 GACATCTGTGTGAAGAGT 4933  
QY 3343 AACTCGATGTCTGTGAGTTCAAGCACTGACTTCTTCAACAGCAAGAGGAGCTTTCAT 3402  
DB 4934 AACTCACTCACTGTGAGTTTCAAGCACTGTGTATCCAGATGCTCCCAATATGAGCACC 5053  
QY 3403 CAATTTTCACTGTGTCAAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3462  
DB 4994 CAGTTTCACTGT 5053  
QY 3463 CGGAGTGTGAGAGT 3522  
DB 5054 CGCTATGAGAGAGAGAGGCTGTGAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5113  
QY 3523 GCGCTGACAGGAAGT 3582

Db 5114 CAGCTCCAAAGGCAAGCAAAATCACCTGTGTGACGTGAATTAACGGGTTCTTTGGCAA 5173  
Qy 3583 CCCAGCCCCGCAATGATCGCTCCCTGCGGGGAGACTGACAGGACCATTTGGAGTC 3642  
Db 5174 CCAGACCTCTCTAATGATAGCTGTGTGGAGGAAATCTGACGGGCCACGAGGATGTT 5233  
Qy 3643 ATCTCTCAACCAATTAACCGAACCCTACCGCCCAAGGAGAGTGTGACTGGAAGTG 3702  
Db 5234 ATTTTGTACCACTAACACAGCCGATCTCTGGGAGGAAATGTGACTGGAAGTA 5293  
Qy 3703 ACCGTCTCAACAGACTAGCTGATGCGCTGTGTATTTAACTTTAACTGAGCCCTGCG 3762  
Db 5294 AAAGTGAACCCGAGACTTTGTGATGCGCTGTATTTAAAGATTTCAAATGAGCCGAG 5353  
Qy 3763 TATGACTTCTCTCAATCTAAGACGAGCGGAGCTCTCTACGCCCTCTCATGAGACTTC 3822  
Db 5354 TATGACTTCTCTCAATCTAATGAAGGAGAAATTTCCAAACAGCCCCCTCATTTGGAGTTAC 5413  
Qy 3823 TATGCTCCAGCTCCAGCGCGCATTTGAAGAGAGAGCAAGCCCTCTCTGCGCTTC 3882  
Db 5414 CAGGGCTCTGAGCCCCGAGAAATAGAGATGAGGAAACAGCTGTTCTGGCAATT 5473  
Qy 3883 CGCAGCGATGATCTGTGAGCAATGCTGCTGTGATGATGATACAGAAACCCGCG 3942  
Db 5474 CGAGATGATGCTCCGTTGCGCTTTGAGGTTGCGCATTTGAATTTAAAGAAACACAG 5533  
Qy 3943 GAGTCAATGTTTATCTGCTGATCAATGAGACGAGACGAGGAGGAGTCCGACTGAG 4002  
Db 5534 GAAGCTGTTTATGACCCAGGAAATATATGATGAGGCAAGAGTTGGAACAGACTTCAG 5593  
Qy 4003 CTGGGCTCTCCGCTCACTAATCTGCAAGGGGGCTGACGAATGAGGCACTGAGAC 4062  
Db 5594 CTGGCTCCACATCACTACAGTGTACTGTGGCTATGAATTTTGAACCTTATTC 5653  
Qy 4063 CTGAGCTGATCTCTGGGGCTGTGAGGAAGCCGTGTGAAACATCCCGGCACTGTC 4122  
Db 5654 ATCACTGTGTATTTGGGGCTGATGGGAAACCTCTCGGGAACAAGTCTGCTCTGCG 5713  
Qy 4123 ACAGCCCCCTGTGGGGAGAGATGTGGGTTGCGAGGAGTGTCTTTGCCCACTAC 4182  
Db 5714 AATGCTCCCTGTGAGGCGCAGTACAGGGGATCAGAAAGGGGTAGTTTATATCAACAACTAC 5773  
Qy 4183 CCCCAGAACTACACAGTGAAGATCTGTGATTTTGTATCTGTGCCCAAGACTAT 4242  
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Db 5834 GTGGTCTTTGGACAGTTTGTCTATTTCCAGACAGCCCTGAATGATTTGGCAGAAATTAAT 5893  
Qy 4303 GACGGCAACAGCAGCACTTGGGGCTCTCAGCTCCCTCTGGGGCTCCCATACAGAGAA 4362  
Db 5894 GATGGAACCATGACACAGGCGCAGACTTCTCAGCTCACTCTCGGGGTCTCACTCAGGGAA 5953  
Qy 4363 TCACTGCTTGGCCACTCTCAATCAAGTTCTATTAAGTTGAGCGCAAGAGCCCTGCG 4422  
Db 5954 ACATTTGCTTGGCTAGTCAAAATCAATTTCTCTCGATTCAGTCAAGAACCGGTGTC 6013  
Qy 4423 CCAGCAGAGGCTTCACTTGTCTACCAAGCGGTTCTTGAACAGCGCAGCGCACTGTC 4482  
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Qy 4483 AGCTGTGTGCGGAACCCGCTATGCGAAGAGGCTGGGAGTACTTCTGCTGGGGGCC 4542  
Db 6074 AGCTGTGTGCGGAGCCAGATACGGAAGGAATTTGTTCTGAGTTTCTGCGGGCTC 6133  
Qy 4543 ATGTGCGCTTCAATGCAATCTCGGCTATGCGCTGAGGGGTGCGCAAGATCACTGTC 4602  
Db 6134 ATGTGCGATTCAGTGAACCCGGGATACCTGCTTCAGGGTTCACAGGGCTCCTGTC 6193  
Qy 4603 CTCCTGTGCTGGGGCTTGGCCCAATGGAATGTCTCAGCGCCCAAGTGTGTGTCGCG 4662

Db 6194 CAGTCCGTGCCCAACGCTTGTGGCACAGTGAAGCAACACCATCCAGCTGTGTGATACC 6253  
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Qy 4723 TACCTCAACAGCCTCACTGTGTGTGGAAGATGTTGTTCCCGAAGGCGCTGGCATCAG 4782  
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Qy 4783 ATCCAAATTTGATGATTTGTGACAGAGCAAACTGGGACTCGCTGAGATTTGATGTT 4842  
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Qy 4843 GCAGATTAACATGTATCAATGCTGTGGGATTTCTAGGAACAAACCGTGTGCTGCTTCG 4902  
Db 6434 GGGGATGTACCGCACCCGAGCTGGAGAACCTTCTAGGACCAACATACCGGACATGCTG 6493  
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Qy 4963 GGCCTTCACTTGTGATGACAAAACGTTGGGCTGTAGAGATTTGTCGGAACCTGCTGTC 5022  
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Qy 5023 AGTAAGGGGTGAAGCTGCGGAGCTTCTGTGGAATGATGTGTGCTTCTGAGT 5082  
Db 6614 AGCAACAGATCAAAATCGGAATCGTATCATGTGGAAGAGCTGTCTCTTCAGTGC 6673  
Qy 5083 GAGCGGGAATGACCTCTCCAGGGGCGCAGCCCATCTCTGATGAGCCGGAACAGTGGG 5142  
Db 6674 GAGCCGGGTAACCTGTGAGGGCGCTTCCACATTTCTGTATGTGCAAGAGACGCTTCC 6733  
Qy 5143 CGATGGAATCACTCTCTCTCACTGTGTATGCAACATGTGTGGGGAACAGTGAAGAGAT 5202  
Db 6734 CGTTGGAATCACTCTCTCTCTCTGTGATGCAACCTGTGAGAGGAGCGCTGAGCACTTG 6793  
Qy 5203 GAGGGGTGATCTGTAGGCCCGGCTTCCAGGCACTACCCAGTAAATGATGATCTGCTCC 5262  
Db 6794 GGTGTGTATCTGTAGCCCGGCTTCCAGGTTCTTACCCCAACATTAAGCTGACCTCACC 6853  
Qy 5263 TGGAAATATGACCTGCGCGGCTTGTGAGCTCACTCAGTCACTGCTGAACTTCTCACC 5322  
Db 6854 TGGAGATCTCACTTACCCATCGGCTATGTGACATATTCAGTTTGTGAATTTTCTAAC 6913  
Qy 5323 GAGCCCAACCAAGATCACTAGAAATCCGAAATGCGCCCTATGACACAGCGCATGAT 5382  
Db 6914 GAAGTAAATCATGACTTCTTGAATTAATTAATGAGCTTTACACACAGCCCATGAT 6973  
Qy 5383 GGAAGATTCAATGGAAGGAGCTTCCAGCTCTCTCTCCACGTTCCACAGACACAC 5442  
Db 6974 GGCATATTTAGGGGCAAGATCTCCCGGCGCTCTGTAGAGCAACAGCATGAACCTTC 7033  
Qy 5443 GTGATTTTCAACAGGACCACTCCGGAATCGGCGAGATTAAGCTGAGATTCAGGCC 5502  
Db 7034 ATTCATTTTATATGATCACTTGTGCAAAACCGGAGATTTTAATTTTGTCTTCAAGCC 7093  
Qy 5503 TATGAATTTCAAGAGTGGCCAGACCCAGAGCCCTTTGCCAATGCAATTTGAGGGAGCT 5562  
Db 7094 TATGAATTTCAAGAGTGGCCAGATTCACCCCATTTCAAAATGGGATGATCACTCG 7153  
Qy 5563 GGTTCACAGTGGGACATGATGATCTTGTGAGTGTCTCCGGGGTATCAATTTGACTGTC 5622  
Db 7154 GATTAAGAGTGGGGCAATCAGATCTTTCGAGTGTATCTGAGGATCAATTTCAATGAGC 7213  
Qy 5623 CACCTGTCTCAACGTTCAACATGAGCAACACCGGAATGAGGACACCCCTGCGCAAG 5682  
Db 7214 CATCTGTCTCACTTGTGATGATGAGATCAACAGAAATGGAATCACTCTTTTCCAA 7273  
Qy 5683 TGTGAATCTCTTGTGCGGGAACATCACTTCTTCCACAGGCACTGTGTACTCCCGGG 5742  
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Qy 5743 TTCCCTAGCCGCTCTCCAGCTCCAGGACTGTGTGGCTGATCAGCTGCCATTGGC 5802  
Db 7334 TTTCTGATGATGATTCGATCTTCAAGACTGCTGCTTGGCTCATCAGGAGCTCCAGG 7393  
Qy 5803 CATGCGCTCCGCTTCAACCTCAGCTGTGTGAGACAGAGCCCTTGAGATTTCATCACC 5862  
Db 7394 CACGAGATTTCATCACTTCACTTGTATCAGAGAGCTGTCAACGATTACATTGCT 7453  
Qy 5863 ATCTGGATGGGACACAGCAACAGCAAGGCTGGCTTTCACCCGAGACATGGCC 5922  
Db 7454 GTTGGAGAGCTCCGATCAGACTCAACCCAGCTGGAGTTTCACTGAGCAACAGACC 7513  
Qy 5923 AAGAAAAGTGCAGAGTTCATCCACAGGCTCTCAAGTTCCACCGTGAATGAGCC 5982  
Db 7514 CTCGAAACGGGCTATGACTCCACCAACAGGCTCTCAAGTTCCACAGGACTTTTCA 7573  
Qy 5983 ACAGGGGGGATCTTGGCATAGCTTTCTCGGCTTA 6017  
Db 7574 AATGAGGCTTCTTGTCTTCATTTCCAGGCTCA 7608

## RESULT 6

US-10-276-934-3  
; Sequence 3, Application US/10276934  
; Publication No. US20030180750A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Leeds  
; APPLICANT: Markham, Alexander F.  
; APPLICANT: Jackson, Andrew P.  
; APPLICANT: Woods, Christopher G.  
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases  
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; CURRENT APPLICATION NUMBER: US/10/276,934  
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; PRIOR FILING DATE: 2001-05-21  
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; PRIOR FILING DATE: 2000-05-20  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 6409  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (588)..(588)  
; OTHER INFORMATION: "n" is any nucleotide  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (624)..(624)  
; OTHER INFORMATION: "n" is any nucleotide  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (672)..(672)  
; OTHER INFORMATION: "n" is any nucleotide  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (2265)..(2265)  
; OTHER INFORMATION: "n" is any nucleotide  
; NAME/KEY: misc.feature  
; LOCATION: (6387)..(6387)  
; OTHER INFORMATION: "n" is any nucleotide  
US-10-276-934-3

Query Match 26.4%; Score 2671; DB 15; Length 6409;  
Best Local Similarity 66.8%; Pred. No. 0;  
Matches 3895; Conservative 0; Mismatches 1854; Indels 84; Gaps 3;

Qy 185 TAACCTAGCTGTGTGTCCCAAGACATTAATATGTCTCAGACCTGTGCATACCCGAAA 244

Db 236 TGAACCAAGAGGTGTTCATTGCTCTGACATGTCTCAAGATCTGGATTCCAGAAA 295  
Qy 245 GGGGCAAAAAGACTAGAGCTCGAATTTTCAGATTAGATCCAGCGTCCAGTTCACTGCAACG 304  
Db 296 ATGTATGAAGACAGAGTTTCCGACTTCAGGTTGGTGCAAAATGTACAGTTTTCATGTAGG 355  
Qy 305 AAGGCTATGACTCTGCAAGGTTCCAAAGGATCACTGTATGAAGTGAAGCAATGTTTG 364  
Db 356 ACAATTAGGTGTCCAGAGGATCTTAAGCATCACTGTCAAGAGATTCAAGAGAGCTTCG 415  
Qy 365 CGGCTTGAGAGCACACAGCGAGCTGTGCGAGCCGAGTGTGATGATCCCACTTCGAG 424  
Db 416 CTGCTTGAAGTACACACAGGCCCATCTGCCAGAGAACATGTGATTCATCTGCTG 475  
Qy 425 GCCCTCGGGATATCATCCTTCCCAATTTCCCATTCAGTATGACAAACAATGACACT 484  
Db 476 GGGCCAGGGGATCATCTCCCTAATTTATCCGGTTCAAGTATGAAGTATGACACT 535  
Qy 485 GTGTGTGATCATCAAGCACTCAACCCCTCAAGTGTATGATGAGCTGGCTTTAGAGAT 544  
Db 536 GTGTGTGATCATCAACACAGCGAGCCGAGCAAGGATCATCAAGCTTGTTCGAAAGAT 595  
Qy 545 TTGATTTGAGAGGGGCTATGACACCTGACGCTGCTGTGATGTGTGATGAGAGGAGCC 604  
Db 596 TTGAGCTGAGCGAGGCTATGACACCTTACGTTGTGATGTGAGAGAGTGGAGACA 655  
Qy 605 AAGAACAGTTCTTCACTGTCTCAAAATGCTGCACTGACAGCCCTCACACCCAGGCT 664  
Db 656 CCAATGCGCTTGTATGATGCT-----CACGGAT 685  
Qy 665 CTCGCATCCAGAGAGCATGCTGGGAGCATCTGAGAGCAGAAATGAGACTGTATGAGA 724  
Db 686 CCAATGTTCTCGACTTAT---TGTGACATGAGACCAAGATGTGCTTACATCTGAGT 742  
Qy 725 TCTGTCTGACATTAGGAGTTCAGATGCAAGTCAAGTTCACTGAGAGAGTCTCAAGA 784  
Db 743 CGATGATGACATTGGC----- 759  
Qy 785 CTCTATATGTGTGAACTTGTGCTCTCTGGACAGATTCAGACAGGCACTTGGG 844  
Db 760 -----TACCTGGGTTTAAAGCTGTTTAAACCAAAATGAAAAGGGGCTGTGGG 811  
Qy 845 ACCCTGCAATACCTGCTATATGCGGAGGAGAGGCTCCGCTTCAACAGGTGACAC 904  
Db 812 ATCTGGAATCCCGGCTATGAGAGCGAGCGAGCTTCTTCATGAGATAC 871  
Qy 905 TCAAGTTGATGTCAGCCGCTTTGAGCTGTGAGAGAGCAATTCATGCCAA 964  
Db 872 TCACCTTTGATGCCGCGGCTTTGAGCTGTGAGAGAGAGATTCACCTGTCAAG 931  
Qy 965 AGAATAACCAATGCTGGGCTAAGAGCCAGGCTGCGTCTCTGCTTCTTCACTTCA 1024  
Db 932 AGAACATCAGTGTGTGCAACAGCCAGCTGTATTTTCATGTTCTTCACCTTAA 991  
Qy 1025 CAGCCGCTGTGGGTTGCTGTCTCCCACTACCAAGAGACTATGCAACCACTCC 1084  
Db 992 CGGATCATCTGGGATTAATCTGTACCAAAATTCACAGGAATATGGAACACATGA 1051  
Qy 1085 ACTGTCTGTGCTCATCTGCGAGGCTGAGAGCCGATTCACCTGTGAGAGCA 1144  
Db 1052 ACTGTCTGTGATTAATCTGAGGCCAGAAAGTCACTTAATCTTAAATGAT 1111  
Qy 1145 TTGACGTGAGCCTCAGTTGATTTCTGTGATCAAGAGTGGGCAACCGCGAGGCG 1204  
Db 1112 TTGATTTGAGCCTCAATTTGACTTCTGCGGTCAAGATATGACATTTTTCATTA 1171  
Qy 1205 CGGCTGTGGCACTTTCAGAGAAACAGCTTCCCTCTTCATCAAGAGAGTGGCCAG 1264  
Db 1172 CTGTCTGTGGTACTTTTCTGCAATGAGTCTTCCAGTGGCAGAGTGGGCA 1231  
Qy 1265 TGGCCGCTGTGAGTTTCAAGTACACTCAACAGGAAAGAGGGCTTCAACATCACT 1324  
Db 1232 TAGTTGCTTGAATTTCACTGACATTCACATCACTGAGAGGGTTCAACATCACT 1291

QY	1325	TTACACCTTCCGACACAAACAGAGTCCCGGATTCGGGGCTTCAGATAATGGCAAAAGCT	1386
Db	1292	ACACCACTTTTGGTACAGATAGTGCCATGATCTCGGACATTCCTATAACGACGACGCTT	1351
QY	1385	TTGGGGACAGGCTCCAGCTGGGACAGCTCATCTCCCTCTCTGTGATGAAGGCTTCCTTG	1444
Db	1352	TTGGTGAACAGGTTTCTACTCGGGAGCTCGGTTTTCTTTCACCTGTGATGATGGCTTTGCA	1411
QY	1445	GGACTCAAGGCTCAGAGNCATACCTTCCGTCCTGAAGAGGGCAGCGTGGTCTTGAAACA	1504
Db	1412	AGACCCAGAGATCCGAGTGCATATCTGCATATCTGCAAGACGGGAACGTGTCTGGAGCT	1471
QY	1505	GGCGTGTGCTCGGAGTGAAGCTCCCTGTGGTGGTCACTGACTTCGGCCAGCGGACCA	1564
Db	1472	CCACCGTGGCCCCGCTGTGAAGCTCATGTGGTGAACCTGACAGCGTCCAGCGGAGTCA	1531
QY	1565	TCCTCTCTCGGGGCTGGCTGGCTTCTAACAAGATGCTTGAAGCTGTGCTGGGTATGG	1624
Db	1532	TTTTGGCTCTCGATGGCCAGAGATTTATTAAGGATTTCTTTCATGTGTAAGGATTAATGG	1591
QY	1635	AGGCCAGCCAGGCTACCCCATCAAAATCACCTTCGACAGATTCAAAACGAGATCACT	1684
Db	1592	AAGCAAAACAGGCGACCTATCAAAAATACTTTGACAGATTCACGACAAGGTCAAAT	1651
QY	1685	ATGACACCCCTGGAAGTACGCGATGGGCGGAGTCTACTCAGCCGCCCTTGTATCGGGTTTAC	1744
Db	1652	ATGACACTTGGAGGTCAAGATGGGGCAGACGAGTTGTCCTCCCACTGATTCGGCGAGTACC	1711
QY	1745	ACGGGACCCAGGTTCCCAATTTCTCATACGACCAACGACATCACTCTACTCTCTTCT	1804
Db	1712	ACGGCACCCAGGACCCCAAGTTCTCATACAGACCGGGAACTTATGATCACTGTGCTATTTCA	1771
QY	1805	CTACCGACAAGATCACTCGGACATCGGCTTTCAGCTCCGCTATGAGCTTTAAACATGCG	1864
Db	1772	CCACTGACAAACAGCGCTCCAGCATCGGCTTCTCTATCACTATGAGAGTGTGACGCTTG	1831
QY	1865	AGTCAGACCACTGTCTGGATCCAGGAATCCAGTAATGACAAGGCTCATGGGAATGACT	1924
Db	1832	AGTCGGAATTCCTGCTGTGACCCGGGCACTCCCTGTGAACGGCCATATGGCCAGGTTGAGACT	1891
QY	1925	TCTACGTGGGGCGCGGTGTGACCTTCACTGTGACTCGGGCTTACACATAATGATACCGGG	1984
Db	1892	TTGGATCAAGTCCACAGTGAATTTCACTGTGACCCGGGGTACACACTAATGATACGACG	1951
QY	1985	AGCCTCTGAATGTGAGCCCAACTTCCAGTGAAGCCGGGACCTGGCCAGTTGTGAAGCTC	2044
Db	1952	AGCCCTCTGTGTGTGAGAGGAACCAACGATGGAACAGCCTTGGCCAGCTGCACGCTTC	2011
QY	2045	TCTGTGTGTGCTTCAATCAAGGCTTCAGTGGACATTTGTGCGCAGGGTTCCCTGACT	2104
Db	2012	TATGTGTGAGGTCTACATCCAGGGAAGATGGAACAGTCTTTCTCTCGGGTTTTCCAGATT	2071
QY	2105	TCTACCCCAACACTGAACTGCACTGTGATTAATGAAACATTCATGAGGAGGTGTG	2164
Db	2072	TTTATCCAAATCTCTTAATCTGCACTGTGACATTAAGTGTCTCTATGTGGAAGGATTC	2131
QY	2165	TCTTCACTTTCACACCTTCCACTGGAAGTGGCCATGACTACTCTCTCACTGACTGGA	2224
Db	2132	AAATGATCTTTCACACCTTTTCACTTGTGAGAGTTCCACGATATTTACTGATCAAGAG	2191
QY	2225	ACGGCAGTTCAACCAAGCCCTGAGAGGCTTAATGTGATCTTCGGCTGCAGCTCCCATCA	2284
Db	2192	ATGGAAGTTTTTCCGAGCCGCTGTGCCAGGCTCACCGGGGTGGGTGTGCTCATACGATCA	2251
QY	2285	GGCGTGGGCTCTATGGCAACTTCACTGCCAGGTCCGCTTATCTCTGATTTTCCATGT	2344
Db	2252	AGGCAGGCTCTGTGTGGAATCTTCACTGCGCAGCTTCGGTTTATATACACTTTCATATT	2311
QY	2345	CATATGAAGATTCACATCACTTCTTAGAGTACGACTTGGAGCCTGTGAGAGCCCG	2404
Db	2312	CGTACGAGGCTTCATATTCATTTTACAGATATGACCTGGAGCACTGATATATCTGT	2371

OY	2405	AGGTCGCCAGCCTA	CAGGATCCGGAAAGGGCTTGACGTTGGGCTGGGGCGACACCTTGACCT	2454	
Dp	2372	GAGTCCTCCGCTT	TAGCCCGGAAGATTGGTTTCACTTTGGGTGGAGACCTCTGACGT	2431	
OY	2465	TCTCTCTCTTCC	CGGGTACCGTCTGAGGGGCA	CGGCCGCACTACGTCGCGGGGCA	2524
Dp	2432	TTTCTCTGCTTCT	CGGATATGTTTAGAAGGTGCACCAAGCTTACCTGCTGGGTGGG	2491	
OY	2525	GACGGCGCTGTG	AGCTCCGCTCTCGCCAAAGTGTGTGCTGAAGTGGGAATTCAGTCA	2584	
Dp	2492	GCCCCCGTGTG	AGTGCACCTTCGCCAAGTGTGTGGCCGAATGTGGAGCAAGTGTCA	2551	
OY	2585	CAGGACATCAG	GGGTACTTGTGTCCCCCACTTCCGTGAACTACAATAACATCATG	2644	
Dp	2552	AAGGAAATGAA	AGGAACATTA	CTGCTCCAAATTTTCCATCCAAATTAAGATATATACATG	2611
OY	2645	AATGATCTACT	CTCATCCAGACCAGCCAGGGAAGGAATTCAGCTGAAAGCCAGGCA	2704	
Dp	2612	AGTGTATCTA	TAATAATGAAACAGAACCGGCAAGGGCACTTACCTTAGAACAGAAAGCT	2671	
OY	2705	TCGAATCTCC	GAGAGAGATGTCTCAAGTTATGTATGTCACACACAACA	CTCGCCGTT	2764
Dp	2672	TCCAGCTGTT	TGAAGAGATCTTAAAGGATATATGTGAAAGAACAGTTCCTC	CACGTC	2731
OY	2765	TGCTGGGAGTT	TATAGCATTCTGATGATGTGGGGTGA	CTTTGAAACAGCAATCCAGCA	2824
Dp	2732	CACGTGGGCA	CGTTCACTAAATAATCACTTCGGGGCTGTATCTTAAACAGCAATCTCAATC	2792	
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Dp	2792	ACCTGTGGCT	TAAGATTAAACCAATGATGTGACACCGACCAAGGTTTTCATCTACCT	2851	
OY	2885	TTTTCAGCTT	TGAAC	CTGATCAATATGTAGGACCCAGGAACCCCAAGTTTGGCTAACAG	2944
Dp	2852	ATACCA	GTTTGTGATCTGTAATAATGTAGGATCCGGGCATCCTTA	CTACGAGCTATAGGA	2911
OY	2945	TTTATGATGA	AGGTCATTTTTCAGAGGAC	TCCGTGTCTCTTCACTGTGTGACCTTGATGAA	3004
Dp	2912	TCCGTGATGA	AGGCACTTTACCA	CACTGATGTTCTGTACAGTTTGAAACCCGGGGTACG	2971
OY	3005	GCCGTGGGGG	TAGGAGAGCTGTGTCTGATGTGAGAGCGCGGACCTCGGGACCGGC	3064	
Dp	2972	CCATGCA	TGGCAGCAACCTTGACCTGTTTGAATGAGACAGAGAGTGGGACAAAC	3031	
OY	3065	CTCTGCCAC	CTGTGTGCGCGAGTGTGAGGAGCAGTGAAGGAGAGAGGTGTGCGGGCAGG	3124	
Dp	3032	CAC	TACTTGATAGCGGAATGTGTGTGATCAATGACGCCAATCAGAGAGAA	3091	
OY	3125	TGCTGTCA	CCCGGATATCCAGCTCCATATGAACAATCTTCACATCTGCATCTGACATCG	3184	
Dp	3092	TATGTCC	CCCTGCTATTCACGTCCGATATGCAACAACCTTCACCTGCACCTGGATTTATAG	3151	
OY	3185	AAGGAGAG	CGCGTGCACCATTTGGGTTACATTCCTCGTGTTTGAAACAGAGAGGTTC	3244	
Dp	3152	AGGAGAG	CCCAAGGAACATTAAGCTTCATTTGATTTTTCGAACGAGATGCTC	3211	
OY	3245	ACGAGTGTG	CGCATCTGGGATGGGCTGTGAGACCGGGGTTCTGTAAGAGCTGA	3304	
Dp	3212	ACGACATCT	CAAGGTGTGGAGCGGGCCGATGACATGATACCTCTGTAAAGAGTGA	3271	
OY	3305	GTGGCCGG	CGCTGCCAAGGACCTGTATAGCACTTCAACTCGGTGTCTCTGCAGTTCA	3364	
Dp	3272	GTGGCTCG	CGCTTCCGGAAGACATTCACAGCACTTCAACTCACTCACCTCGAGTTGC	3331	
OY	3365	GCACTGA	CTTCTTACACAGCAAGCAGGGCTTTGCAATTTTCACTGTCCACAGCA	3424	
Dp	3332	ACA	CGACTTCTTATAGCAAGCTGTGCTTCTTCATCCAGTTCTCCACCTCAATTTACG	3391	
OY	3425	CGTCTGCA	TATGACCTTGAGATCCCGGAGATGGGAGTCCGAGTGTGATCAGTTGGGAG	3484	
Dp	3392	CCA	CTTGTAAAGATCCAGATGTGCCCAAAATGACACCCGTATGAGACAGCAGAGAGG	3451	
OY	3485	CCGGC	GACTCACAGTGTCCAGTGTACACCTTGCTTACGCGCTGACAGGAATGACAGA	3544	

Db 3452 CTGAGACACCGGTCACTTCCAGGTGACCTGGCTATCAGCTTCAGAGGCAAGGCCAAA 3511  
Qy 3545 TCAGCTGTGTGAATGAGAAAGGTTCTTCTGGCAGCCAGCCGCAATGATCG 3604  
Db 3512 TCACCTGTGTGACACTAATACCGGTTCTTTGGCAACAGACCCCTCAATGATG 3571  
Qy 3605 CTCCCTCGGGGGAGACCTGACAGAACATCTGGAGCATCCTCTACCAATTAATCCAG 3664  
Db 3572 CTGCTTGTGAGGAACTTGAACGGGCCAGAGGTGTTATTTGTGACCCCACTACCCAC 3631  
Qy 3665 AACCTAACCCGCGAGGAGAGGTGATGTAAGTGAAGTGAACCTCTGACAGACTAGCTA 3724  
Db 3632 AGCCGTATCTCTCGGAGAGAAATGTGACTGAGAGTAAAGTGAACCCGAGCTTTGTCA 3691  
Qy 3725 TCCGCCGTGTATTAATATCTTTAACTGAGAGCTGCTATGACTTCTCTCATATCTAGC 3784  
Db 3692 TCCGCTGTATATTCATAAAGTTTCAACATGAGGCCAGTATGACTTCTTACACATCTAG 3751  
Qy 3785 ACCGACGGAGCTCTCTCAGCCCTCTCATAGAAAGTTTATGCTCCAGCTCCAGCCG 3844  
Db 3752 AAGGGAAAGTTTCCACAGCCCTCATTTGGAGTTTACAGGGCTCTCAGGCCAGAAA 3811  
Qy 3845 GCATTGAAGCAGCAGCAAGCTCTTCTCTGCTTCCGACAGATGATCTGTAGCA 3904  
Db 3812 GAATAGAGATAGCGGAAACAGCTGTTCTGCACTTGGAGTATGCTCTCGTGGCC 3871  
Qy 3905 ATGCTGGCTTCGTATTTGATATACAGAAACCCGCGGAGTATGTTTATCTGTT 3964  
Db 3872 TTTCAAGGTTTCGCAATTTAAAGAAACACAGGAGTGTGTTTGAACCCAGAA 3931  
Qy 3965 CCATCAAGAACGACACAGGGTGGGTCCGACTGAGCTGGAGCTCTCCGTCACTACT 4024  
Db 3932 ATATATGATGAGAACAGAGTTGAAACAGACTTCAAGTTGGCTTCCATCACTACC 3991  
Qy 4025 ACTGCCACGGGGCTACGAAGTTGAGGGCACTCGACCTGAGCTGATCTGGGGCTG 4084  
Db 3992 AGGTGACTCTGCTATTAAGATTTCTGACCCCTCATCACTGTGTGATGGGGCTG 4051  
Qy 4085 ATGGAAAGCCCGTGTGAACAATCCCGGCACTGTCAGACCCCTGGGGAGCACT 4144  
Db 4052 ATGGAAACCTCTCTGGAGCAAGTCTGCTCTCGCAATGCTCTCTGTGGAGCCAGT 4111  
Qy 4145 ATGTGGTTTGGACGAGAGTGTCTGTCCCACTACCCCGAAGTCAACAGTGAAC 4204  
Db 4112 AACAGGGATCAGAAAGGAGTGTATTCACCAACTACCCCATATTAACAGCTGTC 4171  
Qy 4205 AGATCTGCTGTATTTTGTACTGTGCCCAAGACATATGTGTGTTGGCCAGTTGCT 4264  
Db 4172 AATATGCTCTATTCATCAGGTACCAAGAAATTCGTGTCTTTTGAACAGTTGCT 4231  
Qy 4265 TCTTTCACAGGAGCCCTCAACAGAGTGTGAGGTTTCAAGACGGCAACAGCACTGCG 4324  
Db 4232 ATTTCCAGACACCCCTGAAATGATTTGGAGAAATTTATGATGAACCATGACAGGCCA 4291  
Qy 4325 GCGTCTCAGCTCTCTCTGCGGCTCCCATACAGAGAAATCACTGCTTGGCCACTTCA 4384  
Db 4292 GACTTCTCAGCTCACTCTCGGGGTCTCACTCAGGGGAAACATTTGCTTGGTACGTCA 4351  
Qy 4385 ATCAAGTTCTCATTAAGTTCAAGGCAAGGCTCTGACACAGCCAGAGGCTTCCACTTG 4444  
Db 4352 ATCAATTTCTGCTCCGATTCAGTGAAGAGGAGGCTCTGCGCGGCTTCCACTTGC 4411  
Qy 4445 TCTACCAAGCGGTTCTCGAACAGCGCAGCAGTGCAGCTGTGTGCGGAAACCGGCT 4504  
Db 4412 TGTATCAAGCTGTTCTCTGTATCACTGACACCCATGAGCTGTCTCCCGAGCCAGAT 4471  
Qy 4505 ATGGCAAGAGGCTGGGCACTGACTTCTGCTGGGGGCACTGTCTGCTTGCATGCAACT 4564  
Db 4472 ACGGAAGAGATTTGTCTGAGTTTCTGCGGGCTCATGTCGATTCAGATGCAACC 4531  
Qy 4565 CCGGCTATGCTCTGAGGGGTGACAGATGATGATGCTCTCTGTGCTGGGGCTTGG 4624  
Db 4532 CCGAATACCTGCTTCAAGGTTTCCAGGGCTTCCACTGCACTGCGCAAGTCCGTGCCAACGCTTGG 4591  
Qy 4625 CCCAATGGAATGCTTCAAGCGCCACGTTGTGTGTCGCTGTGAGAGCAACCTCAGAGC 4684  
Db 4592 CACAGTGAAGAGACAGATCCCGAGCTGTGTGATCCTTCAGTGGCAATTTCACTCAAC 4651  
Qy 4685 GAGGGGCAACATCTCTGCTCCCTGCTTCCAGAGCCGTACCTCAACGCTCACTGTG 4744  
Db 4652 GAAAGAGTACATCTGTGCTCCCGCTACCTGTAGCCATACGAAACAACTTGAACGTGA 4711  
Qy 4745 TGTGAAGATGTGTGCTCCGAAAGCGTGCATTCAGATCCAACTTGTGATTTTGA 4804  
Db 4712 TATGAAATCATATGTTGAGAGGCTGGAAATTCAGATCAAGTATCAAGTTTGGCA 4771  
Qy 4805 CAGACAGAACTGGAGCTGCTGAGAGTATTTGATGTGTCAGATTAACACTTAACATGC 4864  
Db 4772 CGAGCAGAACTGGGAGTCTCCCTTGAATTCAGATGTGGGAGATGTACCCACCCAGAC 4831  
Qy 4865 TGGGAGTTTCTCAGAAACACGCTGCTGCTTCTGAAACAGCACTTCAACAGCTCT 4924  
Db 4832 TGGAAAGCTTCTCAGGACCAACAGTACCGGCACTGTGAACAGTATTCACCAACTCT 4891  
Qy 4925 ACTTCATTTTCTACAGATATCAGCGATCTGACGCTGCTTCCACTTGGAGTAAACAAA 4984  
Db 4892 ACTTCATTTTCTACAGATATCAGCGATCTGACGCTGCTTCCACTTGGAGTAAACAAA 4951  
Qy 4985 CCGTGGGCTGAGAGATTGTCGGAACCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 5044  
Db 4952 CTGTAGGCTTCTGCAATGCAAGAACAGACCCCTCCAGCAACAGATCAAAATCGAG 5011  
Qy 5045 AGCGTACTTGTGTAAGTGTGTGCTTCTTCCAGTGTGAGCGGGATATGCTCTCAG 5104  
Db 5012 ATCCGTATGATGTAAGAGAGTGTCTCTTCCAGTGTGAGCGGGATATGCTCTCAG 5071  
Qy 5105 GCAAGGCCACATCTCTGATGAGCCCGGAAACAGTGGCGGATGAACTACCTCTCTCAC 5164  
Db 5072 GCGGTTCCACATTTCTGTATGTCAGAGACCGTGTGAGTATCTGAGCCCG 5131  
Qy 5165 TCTGTATTTGCACTGTGTGGGAAACAGTGAAGAGATGAGGGGATGATCTGAGCCCG 5224  
Db 5132 TGTGATTTGCACTGTGTGGAGGAGCGCTGAGCACTTGGGTGTGATCTGAGCCCG 5191  
Qy 5225 GCTTCCAGGCACTACCCAGTAAACATGAGCTGCTCTGGAATTAAGCACTGCGCTG 5284  
Db 5192 GCTTCCAGGCTTCTTACCCCAACATTAAGTACGCACTGAGAGATCTCTTACCCATG 5251  
Qy 5285 GCTTGGAGTCACTACAGTCTCTGAACTTCTTCCACCGAGCCCAACAGACTACATAG 5344  
Db 5252 GCTATGTGCAATATTCAGTTTCTGAAATTTTCTACCGAAGCTATCATGACTTCTTG 5311  
Qy 5345 AATTCGGAATGGCCCTATGAGAACAGCCGCAATGATGGAAGATTCAGTGAAGCAGC 5404  
Db 5312 AATTTCAAAATGAGCTTACACACAGCCCACTGATGGAATTTAGGGGACGAGATC 5371  
Qy 5405 TTCCAAAGCTCTCTCTCTCCACGTCACAGAGCAACCGGTATTTTCCACAGGACCACT 5464  
Db 5372 TCCCGGGGCTGCTGAGAGCAACGATGAACCTCTATCCTTTATATGAGCAAT 5431  
Qy 5465 CCGAATGCGGCAAGATTCAGCTGAGTATGAGGAGCTGCTTCAACCTTCAAGTGGCCAG 5524  
Db 5432 CCGAAGAGCGGCAAGATTTAACTTGTACCAAGCTATGATTAACAGAACTGTCCAG 5491  
Qy 5525 ACCCAGAGCCCTTTCAGATGATGATGAGGAGAGCTGCTTCAACCTTCAAGTGGCCAG 5584  
Db 5492 ATCCAGCCCATTTCAAGATGGGTATCATATCACTGATTAACAGCTGAGGCAATCAG 5551  
Qy 5585 TGAAGTGTGAGTCTCCCGGGATATCAATGATGAGGAGCTGCTTCAAGTGGCCAG 5644  
Db 5552 TATCTTGAAGTATATCTGAGTATATTTATGAGGAGCTGCTTCAAGTGGCCAG 5611  
Qy 5645 ATGGCAACACCGGAATGGAACACCCCTGAGCCCAAGTGAAGTCCCTTGTGGGAG 5704  
Db 5612 ATGGGATCAACAGAACTGGAATCACTTCTTCAAGATGATGATGCTTGTGGGATCA 5671

Qy	5705	GCATCACTTTCTTCCAAAGGACGTGTACTCCCGGGTCCCTAGACCCGACTACAGCT	5764
Db	5672	ACGTAACTCTTCAGAACGGACACATCTACTCCCTGGCTTTCGTAGTAGATCCGATCC	5721
Qy	5765	CCCAAGACTGATGTCTGCTGTGATCAACCGTCCATTTGACATGGCGTCCGCTCAACTCA	5824
Db	5732	TGAAGGATGTGATTTGGCTCATCAAGGTGCTCCAGGGCAGGAGTTTACATCAACTTCA	5729
Qy	5825	GCTGTCTGCAGACAGAGGCCCTCTGGAGATTTTATCAACCATCTGGAGTGGGACAGCAA	5884
Db	5792	CCCTGTTTACAGACGGAAAGCTGTCAACGATTCATTTGCTTTTGGGACGGTCCCGATCAGA	5851
Qy	5885	CAGCACCAACGGGCTCGGCGTCTTTCACCCGGAGATGGCCAGAAAACAGTCAAGATTAT	5944
Db	5852	ACTCAACCCCAAGCTGGAGATTTTTCAGTGGCAACACAGCCCTCGAAAACGGCGTATAGCTCCA	5911
Qy	5945	CCAAACCAAGTCTGTCTCAAGTTTCCACCGTGAATGACGCCACAGGGGGATCTTTCGCATAG	6004
Db	5912	CCAAACCAAGTCTGTCTCAAGTTTCCACAGCACTTTTCAAAATGAGGAGCTTCTTTGTCTCA	5971
Qy	6005	CTTCTCCGCTTA	6017
Db	5972	ATTTCACAGTCA	5984

QY	185	TAAGTCAGTTGGTGTCTGTCGCCAAGACATATATGTGTTCGAGACCTTGCGATTACCCGAAA	24.7%	Score 2503.6;	DB 15;	Length 5598;	
Db	236	TGAGCCCAAGGAGGTGTGCATTGTGTCTGTGACATGTGTCCAGATCTGGAGATTCCAGAAA	Best Local Similarity 67.0%;	Pred. No. 0;			
QY	245	GGGGCAAAAGACTAGGCTCGGATTTACAGATTAGAGATCCAGCGTCCAGTTCACTGCAACG	Matches 3646;	Conservative 0;	Mismatches 1714;	Indels 84;	Gaps 3;
Db	296	ATGTGTGAAGAAGCAGGTTCCGACTTTCAGAGGTTGTGTGCAAAATGTACAGTTTTCATGTAGG					
QY	305	AGGGCTATGACTTCGACAGGGTTCGCAAGCGGATCACCCTGTATGAAAAGTAGAGCAGCATGTGTTG					
Db	356	ACAAATTAGTGTCTCCAGGAGATCTTAAAGCATCACCTGTCCAAAGAGTTACAGAGACGCTCG					
QY	365	CGGCGTGAAGGACACACAGGCGCAGTCTGCGAGCCCGCATGTGTGATGCCCACTTGAG					
Db	416	CTGCTGTGAGTGAACCAACAGGCCCATCTGCCAGCGAAGAACTGTGATCCCAATCTGGGTG					
QY	425	GCCCCCTGGGCGATCATCACTTCCGCCAATTTTCCCATTCAGTATGACAACATGCACACT					

Db	476	GGCCACAGGGGGCTATTACCTCCCTTAATATCCGGTTCAAGTATGAATATATGCACT	535
Oy	485	GTGTGTGATATATCAAGACTCAACCCCTCCAAAGTGTATTAAGTCGCCCTTTAGAGT	544
Db	536	GTGTGTGGGTATATACCAACCAAGCCCGCAAGAGTCAATAACTGTGCTTTGAAGGT	595
Oy	545	TTGATTTTGAAGAGGGGCTATATACACCCCTGACGGTCGGTATGTGTGTGAGATGGGAGC	604
Db	596	TTGAGTGTGAGACGAGGCTATGACACCTGACGGTTGGTATGTCTGGAAAGGTGGAGACA	655
Oy	605	AGAAACAGTTCTCTACATGTCTCAAAATGCTTGAAGTGAAGCCCTCAACCCAGGCT	664
Db	656	CCAGATCGSTCTTGTACGCTG-CTCAGCGGATTCAGTGTTCCTGACCTCA-----T	704
Oy	665	CTCGATCCAGAGAGCATGTCTGGGGGACATCTGAGGACAGAAATGAGCTGTACTTGAGA	724
Db	705	TGTGAGCATGAGCAACAGATGTGGCTTCACTGTGATCAGTCCGATGTAGCAATTGGCTCAC	764
Oy	725	TCTGTCTGTGACATTAGCAGTTCAAGTGCMAAGTCAAGTTCAGTAGGAAGTCTCCAAAGA	784
Db	765	TGGGT-----	769
Oy	785	CTTCAATGCTGTGGAAGTTGTGTCTCTGTGGACAGAGATGAGACAGGGCAGTTGGGTG	844
Db	770	-----TTAAAGCTGTTTACCAAGAAATTTGAAAGGAGGGGTGTGGGG	811
Oy	845	ACCCTGGCATATCTGCATATATGGCCGAGAGGAAGGCTCCCGTTCACCAAGGTGACAC	904
Db	812	ATCTCGAATCCCGGCTATGTGGAAGCGGACAGAGATTTCTCCATGAGATATAC	871
Oy	905	TCAAGTTTGAATGTCACAGCCCGCTTTGAGCTGTGTGGACAGAGGCAATCATATCCAA	964
Db	872	TCACCTTTGAATGCCCCGGCGGCTTTTGAAGCTGTGTGGGGAGAGATTATCATCTGTACGC	931
Oy	965	AGAAATACCAATGGTCGGCTAAGAAAGCAGGCTGCGTTCTCCGCTCTTCAACTTCA	1024
Db	932	AGAAATACAGTGTCTGTGGCAACAAGCCAGCTGTATTTTCATGTTTCTTCAACTTTA	991
Oy	1025	CCAGCCCGTCTGGGGTGTCTCTGTCTCCCACTACCCAGAGACTATGGCAACACCTCC	1084
Db	992	CGGATCATCTGGGATTAATTCTGTCAACAAATATCCAGAGAAATATGGAAACAACATGA	1051
Oy	1085	ACTGTGTCTGGCTATCTCTGGCCAGGCTGTAGAGCCGATCATCTGAGCTTTCAACACA	1144
Db	1052	ACTGTGTCTGGTTATATATCTCGAGGCAAGAAATCGAATTCACCTTAATCTTTATATAT	1111
Oy	1145	TTGACGTGAGACCTCAAGTTTGAATTTCTGTGTATCAAGATGGGGCCACCCGAGAGGCG	1204
Db	1112	TTGATGTGAGCTCATATTTGACTTTCTCGGGGTCAAGATGATGCGATTTCTGTACATTA	1171
Oy	1205	CCGTCTGGGCACTTCTCAGAAAAACAAGTTTCCCTCTCTCCATCAACAAGCATGGCCACG	1264
Db	1172	CTGTCTGTGGGTACTTTTCTGGCAATAAAGTGCCTTCCAGCTGGCCAGCATGTGGGCTATA	1231
Oy	1265	TGGCCCGTCTCGAATTCAGACTGACACTCAACAGGAAAGAGGGGCTTCAACATCACTT	1324
Db	1232	TAGTTGCTTGGAAATTTCAAGTCTACCAATTCACATACCTGCAAGAGGTTTCAACATCACT	1291
Oy	1325	TTACCACTTCCAGACAACAACAGATGCCCGGATCTCTGGCGTTCCAGTAAATGGCAACCGT	1384
Db	1292	ACACCAATTTGTGCAGATATAGTGCATATGATCTGTGGATTCCTATTAACGAGACGAGTT	1351
Oy	1385	TTGGGGACAGCTTCAGCTGGGACGTTTCATCTCTTCTCTGTGTATGTAAGGCTTTCCTG	1444
Db	1352	TTGTGTACAGATTCTTACTCGGAGGCTCGGTTTCTTTTCCACTGTGATGANTGGCTTTGTCA	1411
Oy	1445	GGAATCAAGGGTCAAGAACATATCACTGCGCTCTGAAGAGGCGAGCGTGTCTGAAACA	1504
Db	1412	AGACCCAGGATTCGAGATCTATTAATCTGTGCAATCTGCAAGAACGGAAAGTGTCTGTAGCT	1471
Oy	1505	GCGCTGTGTCTGGGTGTGAAGCTCTCTGTGTGTGTCACTGACTTTGGCCACGGGACCA	1564
Db	1472	CCACCGTGGCCCGCTGTGAAGCTCATATGTGTGACATCTGACAGCGTCCAGCCGAGTCA	1531



QY 1565 TCTCTCTCCGGGCTGGGCTGGCTTCTACAAGAGTGCCTTGAAGCTGTCCTGGTGAATG 1624  
Db 1532 TTTTGGCTCTCGATGAGCGCAGAGATATTAAGAGTTCTTTACATTGGAATGGAATATG 1591  
QY 1625 AGGCCCAAGCCAGGCTACCCCATCAAAATCACTTCAGACAGATTCAAAACCGAGGTCAACT 1684  
Db 1592 AAGCAAAACAGGCGCAGCTATCAAAATTAACCTTTGACAGATTTCAGACAGAGGTCAATT 1651  
QY 1685 ATGACACCTCGGAAGTACGGGATGGGGGAGCTTAAGAGCCCTTGAATGGGGTTTACC 1744  
Db 1652 ATGACACTTGGAGGTACAGAGATGGGACAGTTGTCCTCACTGATGGGAGTACC 1711  
QY 1745 ACGGAGCCAGGTTCCCAAGTTCTCATACAGACAGCACTACCTTACCTCTCTCT 1804  
Db 1712 ACGGACCCAGGACCCCAAGTTCTCATACAGACCCGGAACCTTCAATGACTCTCTATTCA 1771  
QY 1805 CTACCGACAGAGTCACTGGGACATCGGCTTCCAGCTCCGCTATGAGACTATAACATGCG 1864  
Db 1772 CCACTGCAACAGCGGCTCAGCATCGGCTTCTCATCTCACTATGAGAGTGAACGCTTG 1831  
QY 1865 AGTCAGACCACTGCTGTGATCCAGAAATCCAGTAATGGAAGCGGTCAATGGGAATGACT 1924  
Db 1832 AGTCGATTCCTGCTGAGATCCGGGCACTCCCTTGAAAGGCACTGCGACGCGTGAGACT 1891  
QY 1925 TCTACGTGGGCGCGCTGGTGAACCTTCACTGAGCTCGGCTACACATTAAGTGAAGCGGG 1984  
Db 1892 TTGGCATCAGGTCCACAGTACTTTCACTGAGTGAACCGGGGTATCACTTAAGTGAAGAG 1951  
QY 1985 AGCCTCGAGGTGAGAGCCCACTTCAGTGAAGACCGGGCCCTGCGCAATTTGAAAGTTC 2044  
Db 1952 AGCCCTCTGCTGTGAGAGAACACACAGTGAACACCGCTTGCCACACTCGAGCGCTC 2011  
QY 2045 TCTGTGGTGGCTTCAATCAAGGCTCCAGTGGAGCACTTGTGCGCAGGAGTTCCCTGACT 2104  
Db 2012 TATGTGAAGGCTATCAAGGAGAGTGGAAAGTCTTCTCTCTGGGTTTCCAGATT 2071  
QY 2105 TCTACCCCAACAACTTGAATGCTGACTGATTAATGAAACATTCATGTCAGAAAGGTTGT 2164  
Db 2072 TTTATCAAACTCTCTAACTGACGTCGACATGAACTGATGTCATGAGGAAGAGTTTC 2131  
QY 2165 TCTTCACTTTCACACCTTCCAGTGAAGAGTGGCCATGACCTCCCTCACTGAGA 2224  
Db 2132 AATGATCTTTTCACTCTTCACTTGAAGATTCCTCAAGCATTAATTAAGTCAAGAGG 2191  
QY 2225 ACGGCACTTCAACCAAGCCCTGAGGACCTAACTGATCTCGGCTGCGACGCTCCATCA 2284  
Db 2192 ATGGAAGTTTTCGAGCCGTTGCCAGGCTCACCGGCTCGGTGTGCTCATAGATCA 2251  
QY 2285 GGGCTGGGCTATAGGCACTTCACTGCCAGAGTCGCTTCACTCTGATTTCTCATGT 2344  
Db 2252 AAGCAGGCTGTGTTGAAACTTCACTGCCAGCTTGCTGTTATATCAACTTCTCAATTT 2311  
QY 2345 CATATGAAGATTCAACATCACTTCTCAGATAGATGACTTGAAGCCCTGTGAGAGCCG 2404  
Db 2312 CATAAGAGGCTTCAATATCACTTTTGAATATGACTGAGCACTGATGATGATCTCTG 2371  
QY 2405 AAGTCCCAAGCTTCAAGATCCGAAAGGCTTCACTTGGCGTGGGCAACCTTGAAGCT 2464  
Db 2372 GAGTCCCTGCTTCAAGCCGAAATTTGTTTCACTTGTGTGGGAGACCTCTGAGCT 2431  
QY 2465 TCTCTGCTTCCCGGGATACGCTGAGAGGCAACGCCCGCATCACTGCTGGGGGCA 2524  
Db 2432 TTTCTGCTTCTGGGATATCTTTTGAAGGTCACCAAGCTTACCTGCTGGGGTGGG 2491  
QY 2525 GACGCGGCTGTGAGCTGCTCTGCAAGGTGTGTGCTGAGTGGGAATTCAGTCA 2584  
Db 2492 GCGGCGGTGTGAGTGAACCTTGCAGAGGTGTGTGGCCGATGTGAGAGCAAGTGTCA 2551  
QY 2585 CAGGCACTCAGGATCTTGTGCTGCCCAATTTCTGTGAATCAATTAACATCATG 2644  
Db 2552 AAGGAAATGAAGAACATTAAGTCTCCAAATTTTCCATCAATTAATTAACATG 2611

QY 2645 AATGATCTTATCCATCCAGACCCAGCGAGAGGAATTCAGTGAAGCCAGGAGT 2704  
Db 2612 AAGTATCTATTAATAAGAAACAGAGCCGCGAAGGGCATCCACTTGAACACAGAGCT 2671  
QY 2705 TCGAATCTCCGAAAGAGATGCTCAAGGTTTATGAGGAAACAACATCCGCCGCTT 2764  
Db 2672 TCCAGCTGTTGAGAGAAATACTTAAGGATATGATGAAAGAAACAGTTCTCACTC 2731  
QY 2765 TGCTGGAGTTTAAAGCATTCAGATGATGGGGGTGACTTTGAACAGCATTCAGCA 2824  
Db 2732 CACTGGGACGTTCACTAAATGAATCTTGGGGCTGATCTTAAACAGCATCAATC 2791  
QY 2825 GTGTGGCTGATTTCACTCACTGATGTAATAACAGCAAGGCTTTGAATGCACT 2884  
Db 2792 AACTGGCTGAGTTCAACCAATGATGACACCGAACCAAGTTTCACTCACT 2851  
QY 2885 TTTCCAGCTTGAATCATCAATATGAGAGACCCAGAACCCCAAGTTGGCTTCAAG 2944  
Db 2852 ATACCAATTTGATCTGTAATAATGTAGATCCGGGATCTTACAGGCTATAGGA 2911  
QY 2945 TTCAATGAAAGTCAATTTTGCAGAGAGCTCGTCTCTTCACTGATGACCTGGAATCA 3004  
Db 2912 TCCGATGAAGGCGCACTTTACGACACTGATGTTCTGTACAGTTGCAACCCGGGATACG 2971  
QY 3005 GCTGCGGGGTATGAGAGAGCTGCTGTGATGAGAGAGCGGCGGACCTGGGACCGGC 3064  
Db 2972 CCAATGATGAGCAACACCTTGACTGTTTGAATGAGACAGGAGTGTGGACAAC 3031  
QY 3065 CTGCGCCACTGTGTGCGCGAGTGTGAGAGGACATGAGAGAGAGTGTGGGGAGG 3124  
Db 3032 CACTACCTTGATGATAGCGGAATGTGTGTGATCATGAGCCATCAAGAGAA 3091  
QY 3125 TGCTGTAACCCGGGTATCCAGCTCCCTATGAACAATTCATGATTCGACATGCG 3184  
Db 3092 TATGTCCCGGTATCCAGCTCCGATATGACAAACCTCACTGACCTGGAATTAAG 3151  
QY 3185 AAGCAGAGCGCGGTGACCATTTGGGCTACATTCCTCGTGTGATGACAGAGAGGTTG 3244  
Db 3152 AAGCAGACCCAGAAACATTAAGCTTCAATTTATGTTTTCAGACGGAATGAGCTC 3211  
QY 3245 ACGAGTGTGCGGATTTGGGATGGGCTGTGAGAGCGGGGTTCTGCTGAAGAGTGA 3304  
Db 3212 ACGACATCTTCAGAGTCTGGGAGCGGGCGGTGACAGTGCATCTGTAAGAGTGA 3271  
QY 3305 GTGGCCCGGCGCTGGCCCAAGACCTGATAGCACTTCACTGGTGTCTGCAATTC 3364  
Db 3272 GTGGCTCGGCTTCCGAGAGATCAACAGACCTTCACTCACTCACTCAATTTG 3331  
QY 3365 GCACTGACTTCTTACACGAGACAGGCGTTTGCATTCATTAATTTGATGTCACAGCA 3424  
Db 3332 ACAAGCACTTCTTATCAGCAAGTGTGGCTTCTCCATCCAGTTCTCACTCAATTTG 3391  
QY 3425 GGTCTGCAATTAACCTTGGGATTCGCGGAAATGGAGTGGAGTGTGACATTTGGGAA 3484  
Db 3392 CAACCTGAATCAATCAAGATATGCCCAATATGCAACCCGCTATGAGACAGAGAGAG 3451  
QY 3485 CCGGCACTCCAGAGTTCAGATGAGACCTTGGCTACAGGCTGCGAGGAGTGCAGAG 3544  
Db 3452 CTGAGACACCGTCACTTCCAGTGTGACCTTGGCTATAGCTTCAAGAGCAAGCAAC 3511  
QY 3545 TCACTGTGTGAAGATGAGAACAGGTTTCTTGGAGCCAGCCGCGCAACATGATCG 3604  
Db 3512 TCACTGTGTGACGTGAATTAACGGGTTCTTTGGCAACAGACCTCTATAGTATAG 3571  
QY 3605 CTCCCTGGGGGAGACCTGACAGACCATCTGAGATCTCTCTCAACAAATTAACCA 3664  
Db 3572 CTGCTGTGAGAGGATCTGAGCGGCGCAGAGGTGTTATTTTGTCAACCAACTAC 3631  
QY 3665 AACCTTAACCGCAGAGAGAGTGTGACTGGAAGAGTCCGCTCAACAGACTAGCTCA 3724  
Db 3632 AGCCGATCTCTTGGGAGAGATGTGACTGAGATGAATGAAGCAACCGGACTTTGTCA 3691  
QY 3725 TGCCCTGGATTTAATCACTTTAACTTGAAGCTGGCTATGACTTCTCATATCTAG 3784



Db 3692 TGCCCTGATATTCAAAGTTTCAACATGAGCCCAAGCTATGACTTCTCATCATCATCATG 3751  
 QY 3785 ACGGAGGGAGCTCTCTCAGCCCTCTCATAGAAAGCTTCTATGCTCCCACTCCAGGCC 3844  
 Db 3752 AAGGGAGAGTTTCAACAGCCCTCTATGGAGTTACAGAGGCTCTCAGGCCCGAGAA 3811  
 QY 3845 GCATTAAGACAGACAGACAGCTCTCTCCGCTTCCGACAGATGATCTGTAGCA 3904  
 Db 3812 GAATAGAGATAGCGAGAAACAGCTCTTCTTGGCATTTCCGAGTATGCTCCGTGGCC 3871  
 QY 3905 ATGCTGCTTCTCATATGATATACAGAAACCCGCGGAGTCAATGTTTGTATCTGTT 3964  
 Db 3872 TTTCAAGGTTCCGCTATGATTTAAAGAAACACAGGAGCTTGTTTTGAACCGAGAA 3931  
 QY 3965 CCATCAAGAACGACACAGGAGTGGGCTCCGACTGAAGCTGGGCTCTCCGTCACTACT 4024  
 Db 3932 ATATAATGATGGAGAACAGAGTTGGAACAGACTTCAAGCTTGGCTCCACATCACTACC 3991  
 QY 4025 ACTGCACCGGGGCTACGAAGTTGAGGGGCACTCGACCTGAGCTGATCTGGGGCTG 4084  
 Db 3992 AGTGTACTCTGCTATAGATTCTTGAACCTCTCATCATCACTGTGTATTTGGGGCTG 4051  
 QY 4085 ATGGAGAGCCCTGTGGAACAATCCCGGCAAGTCTGACAGCCCTGTGGGGAGACAT 4144  
 Db 4052 ATGGAGAACCTCTCGGAGCAAGTGTGCTCCCTCGCAATGCTCCCTGTGGAGGCACT 4111  
 QY 4145 ATGTGGGTTTGGACGAGAGTGTCTTGTCCCACTACCCCGAAGTATACCACTGAGAC 4204  
 Db 4112 ACACGGGATCAGAGAGGAGTATGTTTATCACCAATCACTCCCATTAATACAGCTGTGTC 4171  
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 Db 4172 AATATGCTCTATTCATACAGGTACAGAAAGAAATTCGTGTCTTGAACAGTTGGCT 4231  
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Db 4772 CGAGCAGAACTGGGACTCCCTTGAATCCAGATGATGGGAGTGTGACCCGACCCAGAC 4831  
 QY 4865 TGGGGAGTTTTCAGAGAACACCGTGTGCTCCCTTGAACAGACCTCCACAGCTCT 4924  
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RESULT 8  
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 ; Sequence 4, Application US/10276934  
 ; Publication No. US20030180750A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Leeds  
 ; APPLICANT: Markham, Alexander F.  
 ; APPLICANT: Jackson, Andrew P.  
 ; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases  
 ; FILE REFERENCE: 9052-144  
 ; CURRENT APPLICATION NUMBER: US/10/276,934  
 ; PRIOR FILING DATE: 2002-11-20  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/02240  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: GB0012186.3  
 ; PRIOR FILING DATE: 2000-05-20  
 ; NUMBER OF SEQ ID NOS: 16

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Query Match      24.2%; Score 2450.8; DB 15; Length 5667;
Best Local Similarity 67.0%; Pred. No. 0;
Matches 3565; Conservative 0; Mismatches 1671; Indels 84; Gaps 3;

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QY 245 GGGGCAAAAGATGAGCTCGATTTTCAGTTAGATCCAGCTCCAGTTCACTTGCAG 304
DB 296 ATGTGTAAGAGAGAGTGTCCAGCTTCAGAGTGTGTGCAATGTATACAGTTTATGTAG 355
QY 305 AGGGCTATGACCTGCAGAGGCTCCAGCGGATCACTGTATGAAGTGAAGCATGTGTTG 364
DB 356 ACAATTAGCTGTCCAGGGATCTAAAGCATCACCTGTGAGAGATTCAGAGAGCGCTCG 415
QY 365 CGGCTGAGAGCAACCAAGGCGCATGTGCGGAGCCCGCATGTGTGATGCCACTTTCAG 424
DB 416 CTGCTTGAAGTACCAAGGCCCATCTGCGAGCGAACAATGTGATTCATCTGCGTG 475
QY 425 GCCCTCGGGCATCATCACTCCCAATTTCCCAATTCAGTATGACAACAATGACACT 484
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DB 536 GTGTGTGATCATCAACCAACCAAGCGGATCAAGCTTTCAGTTGCTTNGAAGT 595
QY 545 TTGATTTGAGAGGGGCTATGACACCTTGAAGCGGTGAGTGTGTGATGATGAGTGGGAGC 604
DB 596 TTGACTGAGAGGAGCTATGACACCTTGAAGCGGTGAGTGTGTGAGTGGGAGGAGCA 655
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DB 656 CCAAGATCGTCTTGTATNGTCT-----CACGGAT 685
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QY 785 CTTTAACTGTGTGAACTTGTGCTCTGAGGACAGATGAGAGGAGGAGTGGCGGTG 844

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DB 812 ATCTGGAATCCCGCTATGAGAAAGGAGCGGAGAGATTTCTCATGAGATGAC 871
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QY 1025 CAGGCCGCTGAGGAGTGTCTGCTCTCCCACTACCCAGAGAGATGAGCAACACCTCC 1084
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QY 1565 TCTCTCTCGGAGCTGAGCTGCTTCTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1624
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QY 1625 AGGCTCAGGAGCTTACCTCAAAATCACTTGAAGATTTCAAAACGAGGTCAACT 1684
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QY 1685 ATGACACCTGAGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1744
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DB 1712 ACGGACCCAGGAGCCCAAGTCTCTATCAAGACCGGAACTTATCTGATTTCA 1771
QY 1805 CTACCGCAAGAGTCACTGAGATCGGCTTTCAGCTCCGCTATGAGATCTTAACTGCG 1864
DB 1772 CCACTGCAACAGGCTCTCAGATCGGCTTCTCTCACTATGAGAGTGTGACGCTTG 1831
QY 1865 AGTCAGACATGCTGTGATTCAGGAATCCCAATTAATGACAGGCTGAGGAATGACT 1924
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OY	1985	AGCCCTTGAGGTGAGGCCCAACTTCAGTGGAGCGGGGCCCTGGCCAGTTGTGAAGCTC	2054
Db	1952	AGCCCTCTGTCTGTAGAGGAAACACCACTGGAAACACGCTTGCCAGCTGCAGCGCTC	2011
OY	2045	TCTGTGTGGCTTCATTCMAAGCTCCAGTGGGACCATCTTGTGGCAGAGTTCCCTGACT	2104
Db	2012	TATGTGAGGCTACATCCAGGAAAGATGGAAACAGTCTCTTCTCTCGGTTTCCAGATT	2071
OY	2105	TCACCCCAACAATTGAACTGCACTGCACTGGAATGGCCATGACTACTCTCTCATCTGAGA	2224
Db	2072	TTTATCCAACTCTCTAACTGCACTGCACTGGAATGGCTCTCATGGAAGAGATTCTC	2131
OY	2225	ACGGCAGCTTCAACCCAGCCCTGAGGCACTTACGTATCTCGCTGCGACCTCCCATCA	2284
Db	2192	ATGGAAGTTTTCGAGCGCCGTGCGACGCTCACCGGGCTCGGTGCTCATGACATCA	2251
OY	2285	GGCGTGGGCTCTAATGGCAACTTCACTGGCCAGTCCGGCTTATCTGTAATTTCCACATG	2345
Db	2252	AGCAGGCGCTGTGGAATCTTCACTGCCAGCTCTGGTTTATATCAGACTTCTCATAATT	2311
OY	2345	CATATGAAGATTCAACATCACCTTCTCAGATGACACTTGGAGCCCTGTGAGAGCCCG	2404
Db	2312	CGTACGAGGGCTTCAATATCACTTTTACAAATATGACTCGAGCCATGATGATCTCTG	2371
OY	2405	AGTCCCAAGCTTACAGCATCCGGAAAGGCTTGCACTTGGGTGGGCAACTTTGACT	2464
Db	2372	GAGTCCCTGCTTACGCCGAAGATGGTTTTCATTGTGTGGGAACCTCTGACGT	2431
OY	2465	TCTCTGCTTCCCGGATACCGTCTGAGGAGCACCGCCGATCAGCTCGTGGGGGCA	2524
Db	2432	TTTCTCGCTTCTGGGATATGTTTAAAGGTGCACCAACCTTACCTGCTGGGTGGGG	2491
OY	2524	GACGGCGCTGTGAGCTCGCTCTGCCAAGTGTGTTGCTGAGTGTGGAAATTCAGTCA	2584
Db	2492	GCCGCGGTGTGGAGTGCACCTCTGCCAAGTGTGTGGCCGAATGTGGACCAAGTGTCA	2551
OY	2585	CAGGCACTCAGGGATCTTGTGCTGTCCCCCACTTTCCTGTGACATCAATTAACATATG	2644
Db	2552	AAGGAATGAAGGAACATTACTGTCTCCAAATTTTCCATCCAAATTAATGATTAATCCATG	2611
OY	2645	AATGATCTACTCCATCCAGACCCAGCCAGGAAAGGAATTCAGCTGAAACCCAGGGCAT	2704
Db	2612	AGTGAATCTATAAATATGAACAGAAAGCCGCAAGGGGATCCACTTGAACAGAAAGCT	2671
OY	2705	TCGAATCTCCGMAAGGAATGTCTTCAGAGTTTATATGAGCAACAACATCTCGCCGCTT	2764
Db	2672	TCACGCTTTTGAAGGAGATCTCTAAAGGTATATGAGAAAAAGACAGTTCTCCACGTC	2731
OY	2765	TGCTGGAGTTTATAGCATTCTGAGATGATGGGGGTACATTTGAAACGACATCCAGCA	2824
Db	2732	CACGTGGGAGTTCACTTAATATGAACCTCTGGGGCTGATCTTAACAGCAATCCATATC	2791
OY	2825	GTCGTGGCTGATTTCACTCATGTAGTCTGAAAAACCCAGCAAGGGCTTTGAATGCACT	2884
Db	2792	ACCTGTGCTAGATTCAACACCAATGATCTGACACCGAACCAAGGTTTTCATCTCACTCT	2851
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OY	2945	TTCATGATGAAGTCAATTTTGCAGGAGCTCCGTCTCTTCACTGTGACCTTGAAATCA	3004
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QY	3065	CTGTGCCACACTGTGTGTGCGCGAGTGTGAGAGGGAACAGTGAAGGAGAGGTGTGTGGGGACAGG	3124
Db	3032	CACATACCTTCTGTGCATACCGGAATGTGTGTGTCAATTCATGTACAGCCACATCAGAACGAA	3091
QY	3125	TGCTGTCAACCCGGGATTCAGACTCCCTATGAAACAATTCATCTGACATCTGACATCGC	3184
Db	3092	TATGTGCCCTCGGCTATCCAGCTCCGTATGTAGCAACAACCTCACTGCACCTGGATTATATAG	3151
QY	3185	AAGCAGAAGCCGCTGCAACATTGGGCTACACTTCTGTGTGTGGAACAAGAGAGGTTCT	3244
Db	3152	AGGCAAGACCCACGAAAGACCAATTAGCCTCCATTTCATGTTTGTGACACGAGAGATGTCTC	3211
QY	3245	AAGACGTGTCCGATCTGGGATATGGGCTGTGTGAGACCGGGGTTCTGTGAAGAGCTGA	3304
Db	3212	ACGACATCTTAAGGCTGTGGGACGGGCGGGACAGTACATCTCTGTGAAGAGTGTGA	3271
QY	3305	GTGGCCCGGCGCTGTCCCAAGGACCTGTGATAGACATTTCAACTCGTGTCTCGTCACTTTCA	3364
Db	3272	GTGGTCCGCGCTTCCGAGGACATCCACAGCACCTTCACTCACTCACTCACTCGAGTTGCG	3331
QY	3365	GCATGACTTCTTACCAAGACGAGGCTTTTGCATTAATTTTCAGTGTCCACAGCAA	3424
Db	3332	ACAGGACATTTCTTATCAGCAAGTCTGTGGCTTCTCCATCCAGTTCTCCACCTCAATTTGCG	3391
QY	3445	CGTCTGTGAATGACCTCTGGGATCCCCGAGAAATGGGAATCGGAGTGTGTGACAGTTGGGAG	3484
Db	3392	CCACCTGTAAAGATCCAGGTATGTGCCCAAAATGGCACCCGTATGTGAGACACGAGAGAG	3451
QY	3485	CCGGGCACTCCACAGTGTTCAGAGTGTGACCCCTGTGCTACGGCTGACAGGAAAGTCAAGA	3544
Db	3452	CTGAGAGACCCGTACATTTCCAGTGTACCTGTGCTATCAGCTCCAAAGACAGACCCAAA	3511
QY	3545	TCAGCTGTGTGAAGATCGAAGAACGTTCTTCTGGACAGCCCAAGCCGCAACATGATCG	3604
Db	3512	TCACCTGTGTGCACTGAATTAACCGGTTCTTTTGGCAACAGACCTCTCTTACATGACATAG	3571
QY	3605	CTCCCTGGGGGGAGACCTGACAGGACATCTGTGAGATCTCTGACCAATTAACCGAG	3664
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QY	3665	AACCTTACCCGACAGGCAAGGAGTGTGACTGTGAAGTGAACCGTCTCAACAGACTGCTCA	3724
Db	3632	AGCCGTATCTCTCTGGAGAGGAATGTGATCTGTGAAGTGAAGTAAACCCGGACTTTGTCA	3691
QY	3725	TCGCCCTGTGTAATTTAACATCTTTAACTGTGAGCTGTGCTATGACTTCTCCATATCTAGC	3784
Db	3692	TCGCCCTGTATTTCAAAAGTTTCAACATGTGAGGCCACGTAATGACTTCTTACACATCTATG	3751
QY	3785	ACGACGCGGACTCTCTAGCCCTTCTCATPAGAGCTTCTATGTGCTCCGAGTCTCCAGGCC	3844
Db	3752	AAGGGGAAAGATTCMAAGCCCTCTCATGTGGAGTTTACAGGGGCTCTCAGGCCCCCAAAA	3811
QY	3845	GCATTTGAAGAGAGAGCAACAGCCTCTTCCCTGCGCTTCCGAGAGATGCAATCTGTGAGCA	3904
Db	3812	GAATPAGAGATGAGGAGAAACGCTGTGTTCTGTGSAATTTCCGAGTGAAGAGCTCTCGTGGCC	3871
QY	3905	ATGCTGTGCTTGTGATTTGACTTATACAAAAACCCGCGGAGTCAATGTTTGTGATCTTGTT	3964
Db	3872	TTTCAGAGGTTTCGCAATTGAATTTTAAAGAAACCAAGGGAAGCTTGTTTTGACCAAGAA	3931
QY	3965	CCATCMAAGACGCAACCGGTTGGGTTCCGACTGTAAAGTGTGGGCTCTCTCGTCACTTACT	4024
Db	3932	ATATPATAAGATGGGACAAAGATTGGAACAGACTTCAAGCTGTGGCTCCACATCACTTACC	3991
QY	4025	ACTGCGACCGGGGCTAAGAGTTGAGGAGCACTTCGACCCGTGAGCTGCAATCTGTGGGGCTG	4084
Db	3992	AGTGTGACTGTGGCTATPAAAGATTTTTCACCCCTATCATCACTGTGTATATGGGGCTG	4051
QY	4085	ATGGGAAGCCGTGTGGAACAATCCCGGCGAGTCTCACAGCCCTCTGTGTGGGGAGAT	4144

Db	4052	ATGGGAAACCTCTCTGGAGCAAGTGTCTCCCTCTGCAATGCTCCCTGTGGAGGCACT	4111
OY	4145	ATGTGGATTCCGACGGAGTGTCTTGTCCCCCACTACCCCGAAGCTACACAGTGCAC	4200
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OY	4205	AGATCGCTTGTATTTTGTTCATGTGCGCAAGAACTATGTGGTTTGGCCAGTTCCGCT	4266
Db	4172	AAATATGCTCTATTCATTCACGGGTACAAAGGAATGTGTGTCTTTGGACAGTTTGCTT	4233
OY	4265	TCCTTTCACGCGCCCTCAACGACGTGTGAGAGTTCAACGACGCAACCCAGACTGTGC	4322
Db	4232	ATTTCACGACACCCCTGAAATGATTTGGCAGAAATTAATGATGAACCCATGACAGGCCA	4299
OY	4325	GGCTCCTGAGTCCCTCTCGGGGCTCCCATACAGAGAAATCACTGCCCTTGGCACTTCCA	4388
Db	4292	GACTTCTCAGCTCACTCTCGGGGTCTCACTCAGGGGAAACATTTGCCCTTGGCTACGTCAA	4355
OY	4385	ATCAAGTTCTCATTAAGTTCAAGCGCCAAAGGCGCTGCAACACCAAGAGGCTTCCACTTTG	4444
Db	4352	ATCAATTTCTGCTCCGATTCAATGGCAAAAGAGGGTGTCTGTGCCGGCGGCTTCCATTGCG	4411
OY	4445	TCTACCAAGCGGTTCTCTGAAACAGGCGCCACGCACTGTGACTGTGTGCCGAACCCCGT	4500
Db	4412	TGTATCAAGCTTTTCTCTGTACAGTGAACCCAAATGCAAGCTCTGTCCCGAGCCAGAT	4477
OY	4505	ATGCAAGAGGCTGGGAGATGACTTCTCGGTGGGGGCCATCGTCCGCTCGAATGCAACT	4566
Db	4472	ACGGAAGAGATTTGGTTCTGAGTTTTCGCGGCTCCATGCTCGGATTTGAGTGCACAC	4533
OY	4565	CCGCTATGCTCTGACAGGGGTGCGCAAGATGAGTGTCTCTGTGTCTGGGGGCTTTGG	4622
Db	4532	CGGGATACCTGTCTTACAGGGTTCACAGGCGCTCACTGCAGTCCGTGCCCAACGCGCTTGG	4599
OY	4625	CCCAATGGAATGTCACAGCGCCACAGTGTGTGTGCGCGTGTGGAAGCAACTCACAGAGC	4688
Db	4552	CACAGTGAACGACACAGATCCCAAGTGTGTGTACCTTCAGTGGCAATTTCACTCAAC	4655
OY	4685	GCAGGAGGCAACATCTGTCTCCCTGGCTTCCAGAGCCGTAACCTCAACGCTCAACTGTG	4744
Db	4652	GAAAGAGTACATCTGTCTCCCGGCTACCTGACGCATACGGAACAACTTGAACTGTA	4711
OY	4745	TGTGAAAGTGTGTCTCCCGGAAGCGCTGGCATCAATTCGAATGTGTCAATTTTGTGA	4800
Db	4712	TATGGAAGTCAATGATTCAGGAGGCTCGGGAATTCAGATTCMAATGATCAATTTTGTGCA	4777
OY	4805	CAGACAGAACTGGGACTCGCTGGAAGTATTTGATGTGCAGATTAACCTGTAACTATGC	4866
Db	4772	CGAGCAGAACTGGGACTCTTGAAGTCAAGATGTGTGGGATGTGAACCGACCCCAACAC	4833
OY	4865	TGGGAGTTTCTCAGAAACAAACCGTGTCTGCCCTTGTGAACGACACTTCAACAGCTCT	4922
Db	4832	TGGGAAGCTTCCAGAGCAACACAGTACCGGCACTCTCTAAACAGTACTTCCAAACCAACT	4899
OY	4925	ACCTTCATTTCTAATCAAGATATCAGCGTATCTGACAGCTGGCTTCACTTGGAGTACAAA	4988
Db	4892	AACCTGCATTTCCAGTCTGACATTAATGTGTGGAGCTGTGTGTTTCCACTGTGAATACAAA	4955
OY	4985	CGGTGGGCTTGAAGCAGTTGTCCGAACCTGTGTGCCCAAGTAAACGGGGTGAAGACTGGCG	5044
Db	4952	CTGTAGTCTTGTCTCATGCGCAAGAACAGCCCTCCACAGCAACGATCAAAATCGGAG	5011
OY	5045	AGCGTACTGTGTGAATGATGTGTGTCTTTCATGTGTGAGCGGGGAATATGCCCTCCAGG	5104
Db	5012	ATCGGTACATGTGAACGACGTGTCTCTCTTCAATGTGAGCGGGGTACACCTTCGACGG	5079
OY	5105	GCACAGCCCAATCTCTGCAATGCCCGGAACAGTGTGGCGGAGATGAACATCACTCTCCAC	5164
Db	5072	GCCGTTCCCAATTTCTGTATGCGAAGGAACGTTTCCGCGTTTGGAACTATCGTCTCCCC	5131
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QY	5225	GCTTCCCAAGCACTACCCCAAGTACATGACCTGCTCTGTGAAAAATAGCACTGCCCCGTGG	5288
Db	5192	GCTTCCCAAGGTTCTTACCCCAACAATTAGACTGACCTGTGAGAGATCTCATTTACCACATCG	5251
QY	5285	GCTTTGAGAGCTCACATCCAGTTCCTGTGAACCTCTGCACGAGCCCAACACACATACATAG	5344
Db	5252	GCTATGGTGACATATTTCAGTTTCTGAAATTTTCTACCGAAGCTATATCATGACTTCCTGTG	5311
QY	5335	AAATTCGGAATGGCCCCCTTAGAGACCAAGCCGATAGATGGGAAGTTTCAGTGTGAAGCCAGC	5404
Db	5312	AAATTTCAAAATGGACCTTACCAACCAAGCCCCCAATGATTTGGACAATTTAGCCGCAAGGATC	5371
QY	5405	TTCCAGAGCTCCCTCCTCTCCACAGTCCGACGAGACCAACCGTGTATTTTCCACGACCACT	5464
Db	5372	TCCCCGGGCGCCTCTAGAGCAACAACGATGAACCTTCATCTTTTATGTAGCACTT	5431
QY	5465	CCGAGATTCGCGCAGGATTTCAAGCTGGAGTATCGGGCCTA	5504
Db	5432	CGCAAAACCGGCAAGGATTTAACTTGTCTTACCAAGCTTA	5471

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RESULT 9
US-10-276-934-2
/ Sequence 2, Application US/10276934
/ Publication No. US20030180750A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Leeds
/ APPLICANT: Markham, Alexander F.
/ APPLICANT: Jackson, Andrew P.
/ APPLICANT: Woods, Christopher G.
/ TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
/ FILE REFERENCE: 9052-144
/ CURRENT APPLICATION NUMBER: US/10/276, 934
/ CURRENT FILING DATE: 2002-11-20
/ PRIOR APPLICATION NUMBER: PCT/GB01/02240
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: GB0012186.3
/ PRIOR FILING DATE: 2000-05-20
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 6145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (588)..(588)
/ OTHER INFORMATION: "n" is any nucleotide
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (624)..(624)
/ OTHER INFORMATION: "n" is any nucleotide
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (672)..(672)
/ OTHER INFORMATION: "n" is any nucleotide
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (2265)..(2265)
/ OTHER INFORMATION: "n" is any nucleotide
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (5468)..(5468)
/ OTHER INFORMATION: "n" is any nucleotide
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (6027)..(6027)
/ OTHER INFORMATION: "n" is any nucleotide
US-10-276-934-2

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Best Local Similarity 66.9%; Pred. No. 0;  
Matches 3568; Conservative 0; Mismatches 1678; Indels 84; Gaps 3;

QY 185 TAACTAGAGTTGGTGTGTCCCAAGACATATATGTGTCCAGACCTGGCATACCGGAA 244  
Db 236 TGGCCAAAGAGAGGTGTGCAATGGTCTGTGACATGTGTCCAGATCTCGGATCCGAAA 295  
QY 245 GGGGCAAAAGACTAGGCTGGATTTCAGGTTAGGATCCAGCCGTCAGTTCACTGCAAG 304  
Db 296 ATGGTAGAAGAGAGGTTCCGACTTCAGGTTGGTGCAATGTACAGTTTTCATGTAGG 355  
QY 305 AGGCTATGACCTGCAAGGGTCCAGCGGATCACTGTATGAAAGTAGAGCATGTGTTG 364  
Db 356 ACAATTACGTGCTCCAGGGATCTAAAAGATCACTGTGAGAGATTACAGAACCTGG 415  
QY 365 CGGCTGAGAGCAACAGGCGCAGTCTCCGAGCCGCGATGTGTATGCCACCTTGAG 424  
Db 416 CTGCTTGAGGTGACCAAGGCCATCTCGAGCGAACAATGTGATCCAACTCTGCG 475  
QY 425 GCGCCCTCGGACATCACTCCGCAATTCCCAATTGATGACCAATGCACT 484  
Db 476 GGGCCAGCGGCTATTACTCCCTTAATATCCGGTTGAGTAGAATATGACACT 535  
QY 485 GTGTGTGATCATCAGACACTCAACCCCTCAAGGTGATCAAGCTCGCTTTGAGGAGT 544  
Db 536 GTGTGTGGGTCAACCAACGAGCCGAGCAAGGTCAATCAAGCTTGCTTTGAGAGT 595  
QY 545 TTGATTTGAGAGGGGTATGACACCTGACGCTCGGTGATGTGTGATGAGAGGACC 604  
Db 596 TTGAGCTGAGCGAGCTATGACACCTTACGCTTGTGATGCTGGGAAAGGTGGAGACA 655  
QY 605 AGAAGACAGTTCTTCAATGTCTCAAAATGCTGAGTAGACCCCTCACACCCAGGCT 664  
Db 656 CCAGATCGGCTTGTATGTCT-----TACGGAGT 685  
QY 665 CTCGCATCCAGAGAGCATGTGGGACATCTGAGGAGAGATGAGACTGTATGAGA 724  
Db 686 CCAAGTTTCTGTGACTCAT---TGTAGCATGAGCAACAGATGTGGCTATCATCTGAGT 742  
QY 725 TCTGTGTGACATTAGCAGTTCAAGATGCAAGTTCAGGTTCAAGAGAGTCTCAAGA 784  
Db 743 CGGATGATAGCATGGC----- 759  
QY 785 CTTCTAATGCTGTGAACCTTGTGCTCTGGGACAGAGATCGAGCGAGTGTGGG 844  
Db 760 -----TCACCTGGGTTTAAAGCTGTTTACCAAGAAATTTGAAAGGGGAGTGGGG 811  
QY 845 ACCCTGGACATCTGTGATATGCGCGAGGAGAGCTCCGCTTTCACACGATGACAC 904  
Db 812 ATCTTGAATCCCGCTATAGGAAAGGAGCGGAGCAGATTCTTCATGAGATAC 871  
QY 905 TCAAGTTTGAAGTCAGCCCGCTTTGAGCTGTGTGGACAGAAAGCAATCATGCCAA 964  
Db 872 TCACCTTTGAATCCCGCGCGCTTTGAGCTGTGTGGGAGAGATTATCACTGTGAG 931  
QY 965 AGAATAACCAATGTGGGCTAAGAAAGCAGGCTGCTGTCTCTGCTTTTCAATTCA 1024  
Db 932 AGAACAATCAGGTCTGGCAACAGCCAGCTGTGATTTTCAATGTTCTTCAACTTA 991  
QY 1025 CCAAGCCGCTGGGGTTGTCTGTCTCCCACTACCCAGAGAGCTATGCAACCACTCC 1084  
Db 992 CGGCATCATCTGGGATTTATCTGTCAACAAATTTATCAGAGAAATATGGAAACATGA 1051  
QY 1085 ACTGTGTCTGGCTATCTGAGCAAGCTGAGAGCGGATCACTGGCCTTCAAGACA 1144  
Db 1052 ACTGTGTCTGGATTTATCTCGGAGCAGAGAGTGAATTCATCTTAATGATT 1111  
QY 1145 TTGAAGTGAAGCTCAAGTTGATTTCTGTGTCAATGAAGATGGGGCCACCGCGAGCG 1204  
Db 1112 TTGATGTGAAGCTCAATTTGACTTCTCGCGGTCAAGAGATGAGATTTCAGACATA 1171  
QY 1205 CGCTCTGGGACCTTCTCAGAAACAGACTTCTCTCTCATACAAAGAGTGGCACG 1264

Db 1172 CTGTCTGGGTACTTTTTCTGGCAATGAAGTGTCTCCAGCTGCGACAGTGGGCATA 1231  
QY 1265 TGGCCCGTCTCAGATTCCAGACTGACACTCAAGGAAAGGGGCTTCAACATCACT 1324  
Db 1232 TAGTTGCTTGAATTCAGTCTGACATTTCACTACCTGACAGAGGTTTCAACATCACT 1291  
QY 1325 TTACACCTTCCGACACAAGAGTGGCCGAGTCTGGGCTTCCAGTAAATGCAACGGT 1384  
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QY 1385 TTGGGACAGCTCCAGCTGGGAGCTCATCTCTTCTGTGTGATGAAGCTTCTTG 1444  
Db 1352 TTGTGACAGATTCTTACTCGGAGCTCGGTTTCTTCCATGTGATGATGGCTTTGTA 1411  
QY 1445 GGAATCAGGGCTCAGAGACATCACTGGGTCTGTAAGAGGAGCAGGTGTCTGAAACA 1504  
Db 1412 AGACCAAGGATTCGAGTCAATTACTGTGATCTGTAACAGGAAAGGTGTGAGCT 1471  
QY 1505 GCGCTGTGCGGTGTGAAGCTCCCTGTGTGTGATCACTGACTTGGCCAGCGACCA 1564  
Db 1472 CCAAGCTGCCCGCTGTGAGCTCATGTGTGATCATGTGACAGCTCAAGCGAGTCA 1531  
QY 1565 TCTCTCTCGGCTGGCTGTGCTTCAAGAGATCTTGAAGCTGTGCTGTGATG 1624  
Db 1532 TTTGCTCTGTGATGGCAGATATTATAGGATCTTATCAATGTGATGATATTG 1591  
QY 1625 AGGCCAGCAGCTTACCCATTAATAATCACTTGACAGATTCAAAACCGAGTCACT 1684  
Db 1592 AAGCAAAACAGGCCACTATCAAAATATCTTGAAGATTTCAGACAGAGTCAATT 1651  
QY 1685 ATGACACCTTGAAAGTACGATGGCGGACTTACTCAGCGCCCTTGATCGGGTTTACC 1744  
Db 1652 ATGACACTTGGAGGTCAAGATGGGCAAGCTTCTGCTCCAGTATGGGAGTACC 1711  
QY 1745 ACGGACCCAGGTTCCCGAGTTCTTATGACAGACAGCACTTCACTTCTCTCT 1804  
Db 1712 ACGGACCCAGGACCCAGCTTCTCATGACAGCGGAACTTCAATGATCTGTATTC 1771  
QY 1805 CTAACGACAAAGTCACTGGACATGGGCTTCCAGTCCGCTATGAGACTATAACCTGC 1864  
Db 1772 CCACTGACAAAGCCGCTCAGATGGCTTCTCTCATCAATGAGAGTGAACCTTG 1831  
QY 1865 AGTCAGACACTGTGTGATTCAGAAATCCAGTAAATGAGACGCTCATGAGAAATGACT 1924  
Db 1832 AGTCGATTTCTGTCTGAGACCGGAGATCTCTGTGAACGACATCCGACGATGAGACT 1891  
QY 1925 TCTACGTGGGCGGCTGTGATCACTTGTGATCTGCGGCTACACATTAATGAGCGGG 1984  
Db 1892 TTGGCATCAGGTCCACAGTGACTTTCAGCTGTGACCGGGGTACACATTAAGTGAAG 1951  
QY 1985 AGCTTGTGAGTGTGAGCCCACTTCAATGAGAGCGGCGCTGCGCAATGTGAAAGCTC 2044  
Db 1952 AGCCCTGTCTGTGAGAAACCAACAGTGAACCAACGCTTGCACACTGTGAGCGCTC 2011  
QY 2045 TCTGTGTGCTTCAATTAAGGCTCAGTGGGACATCTTGTGCGAGGTTTCCGTACT 2104  
Db 2012 TATGTGAAGCTTACATCAAGGAGAAAGTGAACAAGTCTTTTCTCTGAGTTTCCAGATT 2071  
QY 2105 TCTACCCCAACAATTGAATGACCTGATTAATGAAACATCTCATGAGCAAGGTGTGT 2164  
Db 2072 TTTATCAAACTCTTAACCTGAGGTGACATTAAGTGTCTATGGAAGAGGATTC 2131  
QY 2165 TCTTCACTTTCCACACTTTCACCTGGAAGTGGCATATGACTTCTCTCATATCTGAGA 2224  
Db 2132 AATGATCTTTTACACACTTTTCAATTTGAGAGTTCACACACTTAATCATGATACAGAG 2191  
QY 2225 ACGGACGCTTACCCGAGCCCTGAGGAGCTTAATGATCTGCGGCTGAGCTCCATCA 2284  
Db 2192 ATGGAAGTTTTCGAGCCGTTGCAAGGCTCAACGGGCTGAGTTTCTCATACATCA 2251  
QY 2285 GCGCTGGGCTATATGCAACTTCACTGCGCAGGTCTGCTCATCTCTGATTTCTCATGAT 2344  
Db 2252 AGGCAAGGCTGTTGGAATCTTCACTGCGCAGGCTTGTATATCAGACTTCTCAATT 2311

QY	2345	CATATGAAGATTTCACATCATCACTTCTCAGAGTAGACACTTGGAGCCCTGTGAGAGCCCG	2404
Db	2312	CGTACGAGGGGCTTCATATATCATATTTTCAGAAATATAGACTGGAGCCATGTGATGTCGTG	2371
QY	2405	AGGCTCCAGAGCTTCAGAGATCCGGAAGGGCTGTGAGTTTGGCGTGGGCCACACTTGACT	2464
Db	2372	GAGTCCCTGCTTCAGCCGAAAGATTGGTTTTCATTGTGTGGGAGACTCTTCGAGGT	2431
QY	2465	TCTCTGCTTCCCCGGGTACCGTCTGAGAGGACCGCCCGCATCACTGCTGGGGGGGCA	2534
Db	2432	TTTCTGCTTCTCGGGATATCGTTTGAAGGTGCCACAAGCTTACCTGCTGGGTGGGG	2491
QY	2525	GAGGGGCGCTGTGAGACTCGCTCTTCCGCAAGGTGTGTGCTGATGTGTGGAAATTCAGTCA	2584
Db	2492	GCGCGGTGTGTGAGATGACCTCTGCGCAAGGTGTGTGCGCCAAATGTGAGCAAGTGTCA	2551
QY	2585	CAGGCACTCAGGGTACTTTGCTGTGTCCCCCACTTTCTGTGAACTCAATTAACATCATG	2644
Db	2552	AAGGAATGAGGAACATTACTGTCTCCAAATTTTCCATCCATTTATATATATACCATG	2611
QY	2645	AATGCATCTTACTTCATCCAGACCCAGCGGAGAGGAATTCAGCTGAAACCCAGGCAT	2704
Db	2612	AGGTATCTATATAAATAGAAACAGAAAGCCGCGCAAGGCATCCACTTGAGACAGAAAGCT	2671
QY	2705	TGCAACTCTCCGAAAGAGATGTCTCCAGGGTTTATGATGGGACAAACAACCTCGCCGCTT	2764
Db	2672	TCCAGCTGTTTGAGAGAGTACTCTTAAAGATTATATGAGAAAGACAGTTCCTCAAGTC	2731
QY	2765	TGCTGGAGCTTTTTCAGCAATTCAGATGATGGGGGTACTTTGAAACAGCATCCAGCA	2824
Db	2732	CAGTGGGCACTGTTCATATAAATGAACTTCGGGGCTGATCTTAAACAGCATCCATC	2791
QY	2825	GTCTGTGGTTTATTTTCATCATCTGATGCTGAAAAACACAGCAAGGGCTTTGAATGACT	2884
Db	2792	ACCTGTGGTAAAGTTCACACCAATGAGTCTGACACCGCAAGGTTTCACTCACTCACT	2851
QY	2885	TTTCCAGCTTTGAACTCATCAATGTGAGAACCCGAAACCCCAAGTTTGGCTACAGG	2944
Db	2852	ATACAGTTTGTATCTGTAAATGTGAGATCCGGGATCTCTTACTAGCGCTATAGGA	2911
QY	2945	TTTCATGATGAAGTCAATTTTGGAGGAGCTCCGTCTCTTCAGCTGTGACCTTGATACA	3004
Db	2912	TCCGATGAAAGGCCACTTTACCGCACTGTATGTTCTGTACAGTTTGACCCGGGGATG	2971
QY	3005	GCCTCGGGGTAGTAGGAGCTGCTGTCTGAATGGAGAGCGCCGCACTGGGACCGCG	3064
Db	2972	CCATGCATGGCAGCAACACCTGACTTGTGATGGAGACAGAGGTGTGGAAACAAC	3031
QY	3065	CTTGCCTCACTGTGTGCGCCGAGTGTGAGGGAACATGAGAGAGAGAGTGTCCGGGACAG	3124
Db	3032	CAGTCACTTCGTGCAATACGGAAATGTGGTGTGATCATGTACAGCCACATCAGACGAA	3091
QY	3125	TGCTATCAACCGGGATATCAAGCTCCCTATGAAACAATTCGAACCTGATTTGGACCATG	3184
Db	3092	TATTTTCCCTGTGGCATCACTGCTCGATGACAACTCCACTGCACTGATATATAG	3151
QY	3185	AAGCAGAGCGCGGTGCACTATTGGGCTACACTTCTGTGTTTGAACAAGAGAGAGTTTC	3244
Db	3152	AGGCAGACCCAGAAAGACATATAGCTTCATTTCAATTGTTTTCGACAGGAATGGCTC	3211
QY	3245	ACGAGTGTCTGGCATCTGGGATGGGCTGTGAGAGCGGGATTTGCTGAAGAGACTGA	3304
Db	3212	ACGATATCTTAAGGTCTGGGACGGGCGGTGACAGTGCATCTGTGAAGAGATGGA	3271
QY	3305	GTGGCCCGGCGCTGCCAAAGGACCTGATAGCACTTGCATGGTGTGACAGAGAGTTC	3364
Db	3272	GTGGTCCGCGCTTCCGAGGACATCCACAGCACTTCAACTACCTACCTCGCACTTCG	3331
QY	3365	GCACTGACTTTTACAGCAAGCAGAGGCTTTGCATTTCAATTTTCAAGTGTCCACAGCA	3424
Db	3332	ACACGCACTTCTCATAGCAAGTGTGGCTTTCATTCAGATTCTCACTCAATTTCAG	3391

QY	3425	CGTCCGCAATGACCTCGGGATATCCCCAGATATGGAGTGTGAAGTGGAGG	348
Db	3392	CAACCTGTAAACGATTCAGAGTATGCCCCAAATGGACCCGCTATGGAGACAGCAGAGAG	345
QY	3485	CCGCGCACTCCACAGTGTCCAGTGTGACCCCTGGACTACGGCTGCAGGGAGAATGGCAGAG	354
Db	3452	CTGAGAGCAACCGTCACATTCAGTGTGACCCCTGGCTATAGTCTCCAAAGAACGCCAATA	351
QY	3545	TCAGCTGTGAAAGATCGAAGACAGGTTCTTCTGGACGCCAGCCCGCAACATGCATGC	360
Db	3512	TCACCTGTGTGACGCTGAAATAACCGGTTCTTTTGGCAACAGACCTCTCATGCATGATG	3572
QY	3605	CTCCCTGCGGGGAGACCTGACAGGACCATCTGGAGTACCTCTCAACCAATTACCCAG	366
Db	3572	CTGCTGTGTGAGAGGAATCTGAAGGGCCAGCAGGTGTATTTTGTGACCAACTACCA	3633
QY	3665	AACCTTACCCGCGCAGGCAAGAGTGTGACTGGAAAGTGAACGCTCTACACAGTACTGTCA	3722
Db	3632	AGCCGTATCTCTCGGGAAAGAAATGTGACTGGAGATAAAGTGAACCCGAGCTTTGTCA	3692
QY	3725	TGCGCCGTGTATTTAACATCTTTAACCTGGAGCCTGGCTATGACTTCTCCATATCTACG	378
Db	3692	TGCGCTGTATTTCAAAAGTTTCAACATGAGAACCCAGCTATGACTTCTTCAACATCTATG	3752
QY	3785	ACGGAACGGGACTCTGTCAAGCCCTCATATGAGAACCTTATAGGCTCCAGACTCCAGGCG	3844
Db	3752	AAGGGGAAGATTCCAACAGCCCCCTCATTTGGAGTTACACAGGCTCTACAGGCCCAAGAA	3811
QY	3845	GGATTGAAAGCAGCAGCAACAGCTCTTCTCGCTTCCGACGAGTCAATCTGTGACA	3904
Db	3812	GAAATGAGAGTACCGGAAACAGCTGTTCTTGAGCATTTCCGAGTGAATCCTCCGTGGGCC	3871
QY	3905	ATGCTGCTTCGTCACTTACTATAACAGAAACCCGCGGAGTCAATGTTTATCTGTGTT	3964
Db	3872	TTTCAGGGGTGGCCATTGATTTTAAGAGAACACACGGGAAGCTTGTTTTACCCAGSAA	3931
QY	3965	CCATCAAGAACGACACAGGCTGGGGTCCGACTGAAGCTGGGCTCTCCGTCACTTACT	4024
Db	3932	AATATATGAATGGGACAGAGTGTGAAACAGACTTCAAGCTTGGCTCCACCATCACTAAC	3991
QY	4025	ACTGCGACGGGGGCTACAGAGTTGAGGGGCACTTGACCCCTGAGCTGCATCCTGGGGCTG	4084
Db	3992	AGTGTGACTCTGGCTATTAAGTATTTTGACCCCTCATTCATCACTGTGTGATTTGGGCTG	4051
QY	4085	ATGGGAACCCCGTGTGAACAATCCCGGCGAGTCTGCACAGCCCTGTGGGGAGAGT	4144
Db	4052	ATGGGAAACCTCTCGGGACCAAGTGTGCTCCTCTCAATGCTCCTGTGGAGGCAGT	4111
QY	4145	ATGTGGGTGGGAAGGAGTGTGTTGTGCCCACTAACCCCAAGACTTACACCACTGAGAC	4204
Db	4112	ACAGGGATCGAAGGGGTATTTTATACCAAACTAACCCCAATTAATTAACAAGCTGTCT	4171
QY	4205	AGATCTGCTTATTTTGTTACTGTGTCCAAAGACTATGTGTGTGTGGCCAGTTCGCT	4264
Db	4172	AAATATGCTCTATTTTCATCACGGTACCAAGGAATTCGTGTCTTTTGACAGTTTGCT	4231
QY	4265	TCCTTTCACAGGCCCCCAAGACGTGTGAGGTTACGACGGCCACAGCCACGACTGCG	4324
Db	4232	ATTTTCAGACAGCCCTGAATGATTTGGCAAAATTAATTTGATGAAACCATGACAGGCCA	4291
QY	4325	GGCTCTCAGTCCCTCTCGGGCTCCCATACAGAGAAATACTGCCCTTGGGCAACCTCCA	4384
Db	4292	GACTTTCAGTCACTTCGGGGGTCTCACTCAGGGGAAACATTGCCCTTGGCTTACGTCAA	4351
QY	4385	ATCAAGTTTCAATTAAGTTACGGCCAAAGGCTCTGCACAGCCAGACAGCTTTCACATTGG	4444
Db	4352	ATCAAAATTTGCTCCGATTCAGTGAAGAAAGAGCGGTCTCTGCGCGGCTTCACTTGG	4411
QY	4445	TCATCAAGAGGTTTCCCTCGAACCAAGGGCCACGAGTGCAGCTTGTGTCCGGAACCCGCT	4504
Db	4412	TGTATCAAGCTTCTCTCGTACCAATGACACCCAAATGACGCTTGTGTCCCGAGCCAGAT	4471
QY	4505	ATGGCAAGAGCTGGGCAATGATCTTCTCGTGGGGGCAATGCTCGCTTCTGAATGCAACT	4564

Db	4472	AAGGAAGAGAAATGGTTCTTGAGTTTCTGCCGCGCTCCATCGTCCGAATTCCAGTGCAC	4531
Oy	4565	CCGGTATGCCCTGAGGGGTGCGCCAGATGAGTGCCTCCCTGCTGGGGCTTGG	4624
Db	4532	CGGGATACCTGTTCAAGGATTCACGGGCGCTCACTGCAGTCCGTGCCAACGCTTGG	4591
Oy	4635	CCCAATGGAATGTCACAGGCCCAAGTGTGTGGCCGTGTGGAGCAACCTCACAGAC	4688
Db	4552	CACGTGGAAACAACGATCCCACTGTGTGTACCTCGAGTGGCAATTTCACTCAAC	4651
Oy	4685	GCAGGGGACCATCTCTGTCCCTGGCTTCCAGAGCCGTACTCAACAGCCTCAACTGTG	4744
Db	4652	GAAAGGTATCAATCTGTCTCCCGGCTACCTGAGCCATPAGGAACAATTTGACTGT	4711
Oy	4745	TGTGGAATCGTGGTCCCCGAAGGCGCTGGCATCCAATCCAAGTTGTCAGTTTGTGA	4804
Db	4712	TATGGAATCATATGTTACGGAGGGCTGGGAATTCAGATCCMAGTGATCAAGTTTGTCA	4771
Oy	4805	CAGAGCAAACTGGGACTCGCTGGAAGTATTTGATGTGAGATTAACACTGTAACTATGC	4866
Db	4772	CGAGACAAACTGGGACTCTCTTGAGATCCAGATGTGTGGGATGTGACCCGACCCAC	4831
Oy	4865	TGGGAGTTTCTCAGGAACAACCGTCTGCTCCCTTTCTGAACGACCTCCACAGCTCT	4924
Db	4832	TGGGAAGCTTCCAGGCAACAAGTACCGGCACTGCTGAACAGTCTTCAACCAACTCT	4891
Oy	4925	ACCTTCATTTCTACATCATATACAGATATCGAGATGTGAGCTGGGCTCCACTTGAAGTACAA	4984
Db	4882	ACCTGCATTTTCAAGTCTGACATTAATGTGGCAGCTGTGGTTTCCACTTGAATACAA	4951
Oy	4985	CGGTGGGCTTGAGCAGTTGTCCGGAACCTGTGTGCCCCAGTAAACGGGTGGAAGCTGGCG	5044
Db	4952	CTGTAGTCTTGCTCATGATGCCAAGAACGAGCCCTCCGACGAAACGATCAAAATCGGAG	5011
Oy	5045	AGCGTACTTGTGTGAATGATGTGTGTCTTTTCCAGTGTGAGCCGGGAATATGCTCTCCAGG	5104
Db	5012	ATCGGTATATGTGTGAACAAGTGTCTCTCTTCCAGTGTGAGCCGGGATACCTTCGAGG	5071
Oy	5105	GCCAGCGCCACATCTCTGTCATGCGCCGGAACAGTGTGGCGAGATGGAATCAACCTCTCCAC	5164
Db	5072	GCGGTCCCACTTTCTGTATGCCAGGGAACGTTGCGCGTTGGAACATACCTGTCTCCC	5131
Oy	5165	TCTGTATTGACAGTGTGGGGGAACGTGAGAGATGAGGGGGTATCTTGAGCCCCG	5224
Db	5132	TGTGATTTGCAACCTGTGGAGGAGCGCTGAGACACTTGGGTGTGTGATCTCTGAGCCCCG	5191
Oy	5225	GCTTCCGAGCAACTACCCAGTAAATGATGAGCTGCTCTGGAAAAATACAGTGGCCCGTG	5284
Db	5192	GCTTCCGAGTTCTTACCCCAACAATTAGACTGACCTTGGAGATCTCATTAACCATCG	5251
Oy	5285	GCTTTGAGCTCACATCCAGTTCTGAACTTCTCCACGAGCCCAACCAACGATACATAG	5344
Db	5252	GCTATGTGACATATTCAGTTTCTGATTTTCTTACCGAAGCTAATCATGACTTCTGTG	5311
Oy	5345	AAATCCGGAATGCCCCCTTATGAGACACACCGCATGTATGGGAAGATTCACTGTGAAGCAGC	5404
Db	5312	AAATTCAAAATGAGACTTACCAACACACACCCCATATTTGACAATTTAGCGGACGAGTGC	5371
Oy	5405	TTCCAGCTCCTCTCTTCCAGTCCACGAGACCAACCGTATTTTCCACAGCAGCACT	5464
Db	5372	TCCCCGGGCGCTGTGAGACAAACGATGAACCTCATCACTTTATATGTGACATT	5431
Oy	5465	CCCAAGATTCGGCAGGATTTCAAGCTGAGATACAGGCTTATGAACTTCAA	5514
Db	5432	CGCAAAACCGGACGAGATTTAAACTTGTCTTACCAAGTATGGAACAAACA	5481

RESULT 10  
US-09-799-514-3  
; Sequence 3, Application US/09799514  
; Patent No. US20020065220A1  
; GENERAL INFORMATION:

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: APPLICANT: Young et al.
: TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and
: FILE REFERENCE: PTO15P1
: CURRENT APPLICATION NUMBER: US/09/799,514
: CURRENT FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: PCT/US00/23662
: PRIOR FILING DATE: 2000-08-29
: PRIOR APPLICATION NUMBER: 60/152,248
: PRIOR FILING DATE: 1999-09-03
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 2487
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-799-514-3

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Query Match	20.9%	Score 2122.4	DB 9	Length 2487
Best Local Similarity	99.0%	Pred. No. 0		
Matches 2135, Conservative	0	Mismatches 21	Indels 0	Gaps 0

OY	6238	TACCTCACAGGCGATGATCTCTAGGCGAAGACTACCTGGAACTATCCCACTTCCAGAC	6529
Db	1	GACTTCACAGGCGTGATCTTAGGCCAGAGCTACCTGGAACTATCCCACTTCCAGAC	60
OY	6298	TGCTCTTGCGCTGTGTAGAGTGGAGCCGCACTATAACATCTCCCTCACAGTGGAGTATTC	6357
Db	61	TGCTCTTGCGCTGTGTAGAGTGGAGCCGCACTATAACATCTCCCTCACAGTGGAGTATTC	120
OY	6358	CTCAGCGAAGAACATATGATGAGTTTGTGATTTTGTGATCCATCAGAACAGAGTCTT	6411
Db	121	CTCAGCGAAGAACATATGATGAGTTTGTGATTTTGTGATCCATCAGAACAGAGTCTT	180
OY	6418	CTGCGTGAAGCCCTCAGTGGGAAATTACCTCAGTCCCGGATTTGTACCAAGCTCAAGAAC	6477
Db	181	CTGCTGAAGCCCTCAGTGGGAAATTACCTCAGTCCCGGATTTGTACCAAGCTCAAGAAC	240
OY	6478	TCTGTGTATCCTGCAGTTGGTTCATCTGATCACCGCTACAATCGAAGGGCTTCAAGATCCG	6533
Db	241	TCTGTGTATCCTGCAGTTGGTTCATCTGATCACCGCTACAATCGAAGGGCTTCAAGATCCG	300
OY	6538	TATTTCAGCCCTTACTGTGAGCTGTGCGCAGGGGCTCACTCAATGGCTTATCTTAAAGCCAG	6599
Db	301	TATTTCAGCCCTTACTGTGAGCTGTGCGCAGGGGCTCACTCAATGGCTTATCTTAAAGCCAG	360
OY	6598	ACCAGCAACCCAGCCCGGGGGGCTCCATCACTTGGGTGCAACGGCGGTACCGGCTGTGTG	6655
Db	361	ACCAGCAACCCAGCCCGGGGGGCTCCATCACTTGGGTGCAACGGCGGTACCGGCTGTGTG	420
OY	6658	GGACACAGACATGAGGCATCTGTATCCCGGACCCCGAGGGCTTACCACTGTGTGAGCGAACC	6711
Db	421	GGACACAGACATGAGGCATCTGTATCCCGGACCCCGAGGGCTTACCACTGTGTGAGCGAACC	480
OY	6718	ATCCCTCTCTGTCAAGCTCTTTCCTGTGGGCTTCTTGAGGCCCCCAAGATGAAATGGTG	6777
Db	481	ATCCCTCTCTGTCAAGCTCTTTCCTGTGGGCTTCTTGAGGCCCCCAAGATGAAATGGTG	540
OY	6778	TTTGGGCAAGAGTATCACAGTGGGAAACCAAGGCCGTGTACACTGTCAAGTGAAGGCTTACAC	6833
Db	541	TTTGGGCAAGAGTATCACAGTGGGAAACCAAGGCCGTGTACACTGTCAAGTGAAGGCTTACAC	600
OY	6838	CTCAGCAGCAGGCGCTGAGGCGCACTGTGACAGATGTCTTGACACAGGCTTATGAGACCAACGC	6897
Db	601	CTCAGCAGCAGGCGCTGAGGCGCACTGTGACAGATGTCTTGACACAGGCTTATGAGACCAACGC	660
OY	6898	AATGTCCCAACCAAGTGTCTCTGTGTACTTGTCTTGTCTGTATGTCAAGTACAGCGTGGAG	6957
Db	661	AATGTCCCAACCAAGTGTCTCTGTGTACTTGTCTTGTCTGTATGTCAAGTACAGCGTGGAG	720
OY	6958	CATGGCCGATGAGAGCTTATCTTTGAGACACAGTATCAGTTCCAGAGCCCACTATATGCTC	7017
Db	721	CATGGCCGATGAGAGCTTATCTTTGAGACACAGTATCAGTTCCAGAGCCCACTATATGCTC	780



QY 7018 ATCTGTGACCTGAGCTACTATATAGGCAAAAGGCTATCCGCTGTGAGCCAAATGGC 7077  
 DB 781 ATCTGTGACCTGAGCTACTATATAGGCAAAAGGCTATCCGCTGTGAGCCAAATGGC 840  
 QY 7078 AAATGAGCTCGGGAGCTCTAGGCCCACTGCGGAATCATCTCTGTGTGAGAGCTCCG 7137  
 DB 841 AAATGAGCTCGGGAGCTCTAGGCCCACTGCGGAATCATCTCTGTGTGAGAGCTCCG 900  
 QY 7138 ATTCCTCCCAATGAGCCAGGATCGGAAACATGTCGTCTAAGGGGCAACAGCAATCTTC 7197  
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 DB 961 TCTGTCAATTCGCGATACACATGTGTGGCTCCAGGGTGGTGTGATGATGAGCAATGG 1020  
 QY 7258 CTCTGAGTGGCTCTGAAATCGCTGCTGTGTGTGAGACCTGTGTGAGAGCTCCGAGCCATT 7317  
 DB 1021 CTCTGAGTGGCTCTGAAATCGCTGCTGTGTGTGAGACCTGTGTGAGAGCTCCGAGCCATT 1080  
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 DB 1081 GTCAAGGACACATCAATGAGGAGAACTACAGCTACCGGGGAGTGTGTGATGATGATG 1140  
 QY 7378 AATGCTGGCTTCGCTGATGAGCATGTCTGTGCGCATCTGCCAGAGATCATCACTGG 7437  
 DB 1141 AATGCTGGCTTCGCTGATGAGCATGTCTGTGCGCATCTGCCAGAGATCATCACTGG 1200  
 QY 7438 TCGGGAGAGACCCCTTCTGTGTGCAATTACTGTGTGACACCCAGGCAACCTGTCAAC 7497  
 DB 1201 TCGGGAGAGACCCCTTCTGTGTGCAATTACTGTGTGACACCCAGGCAACCTGTCAAC 1260  
 QY 7498 GGCCTCACTCAGGGTACCAAGTTTAACCTCAAGATGTGTGATGATGATGATGATG 7557  
 DB 1261 GGCCTCACTCAGGGTACCAAGTTTAACCTCAAGATGTGTGATGATGATGATGATG 1320  
 QY 7558 GGGTATATGCTGAGGGGGCTGTAGGTCCCAATGCTTGGCCAGGGGCAATGAGATGAC 7617  
 DB 1321 GGGTATATGCTGAGGGGGCTGTAGGTCCCAATGCTTGGCCAGGGGCAATGAGATGAC 1380  
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 DB 1561 TGGGACCGTCCCGCCGCGCCAGAGTGTCTGTGTGTGAGGCAATCCGGGCTCCCGGCT 1620  
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 QY 7918 GGCAGAGGATCTGTGTGAGAGAGACGCGCAATGTGTGGCTGTGATGAGACCTGAC 7977  
 DB 1681 GGCAGAGGATCTGTGTGAGAGAGACGCGCAATGTGTGGCTGTGATGAGACCTGAC 1740  
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 DB 1801 GCTCATGAGATCTGTTTGGGGAGACGCTTTGATTCAGGCACTGTGTGATGAGCTGT 1860  
 QY 8098 GAAAGTGGACAGTGTCTCGGGGATGTCAGAGGCGCACTGTCAAGCAATGAGCTGTG 8157

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 DB 1921 ACGGCTCGCAGCCTGAGTGTGAGTGTATCTTGTGTGGAACCCCTGGAGCTCCAGTAT 1980  
 QY 8218 GCCCAGTTGTGTGATGATGAGCTGTGTGTCTTCCAGCTTATATGATGAGTCCG 8277  
 DB 1981 GCCCAGTTGTGTGATGATGAGCTGTGTGTCTTCCAGCTTATATGATGAGTCCG 2040  
 QY 8278 GAAAGTACTAGCAGCAGGCTGTGAGCGGTACCTGCTGTGATGATGATGATGATG 8337  
 DB 2041 GAAAGTACTAGCAGCAGGCTGTGAGCGGTACCTGCTGTGATGATGATGATGATG 2100  
 QY 8338 GGCAGTACCTGAGTGTGTGTATTAATGTGTGTGATGATGATGATGATGATG 8393  
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 RESULT 11  
 US-10-108-260A-814  
 ; Sequence 814, Application US/10108260A  
 ; Publication No. US2004005560A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HELIX RESEARCH INSTITUTE  
 ; TITLE OF INVENTION: No. US2004005560A1e1 full length cDNA  
 ; FILE REFERENCE: H1-A0106  
 ; CURRENT APPLICATION NUMBER: US/10/108, 260A  
 ; CURRENT FILING DATE: 2002-03-27  
 ; NUMBER OF SEQ ID NOS: 5458  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 814  
 ; LENGTH: 3810  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-108-260A-814  
  
 Query March 15.5%; Score 1569; DB 16; Length 3810;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1592; Conservative 0; Mismatches 20; Indels 1; Gaps 1;  
  
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 QY 8479 GTATCTGTGTGAGCTGACCAAGAGCCGAGCATGGAATGAAACCAAGCCGCTGTGCAA 8538  
 DB 61 GTATCTGTGTGAGCTGACCAAGAGCCGAGCATGGAATGGAATGGAACCAAGCCGCTGTGCAA 120  
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 QY 8599 ATGTGGGCTCAAGTGTGATCTTATGCTGCTGTGAGAGGGGTACCAAGCTCTCCCTGCG 8658  
 DB 181 ATGTGGGCTCAAGTGTGATCTTATGCTGCTGTGAGAGGGGTACCAAGCTCTCCCTGCG 240  
 QY 8659 GTGTTCACCTGTGAGGAAATGGGTCTGTGACCGAGAGCTGTCTTATGATGATGATG 8718  
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 QY 8719 TTTCTGCGGGATCTGTGTGTCCGTCGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 8778  
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 QY 8779 AGGTCAATCTGTCTCTTCTCTGCAATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGT 8838  
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QY 8899 ACCAGTGTGGGAGCCCTGGTGTGCAAGTTTGGATACAGAAACAATTCTCAGGGCTAC 8958  
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 US-10-467-042-27  
 ; Sequence 27, Application US/10467042  
 ; Publication No. US20040077048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WARREN, Bridget A.; HONCHELL, Cynthia D.;  
 ; APPLICANT: LU, Yan; CHAMLA, Naxinder K.;  
 ; APPLICANT: BUREFORD, Neil; DELEGEANT, Angelo M.;  
 ; APPLICANT: GANDHI, Ameena R.; BAUGHN, Mariah R.;  
 ; APPLICANT: GRIFFIN, Jennifer A.; GIEZSEN, Kimberly J.;  
 ; APPLICANT: LU, Dying Aina M.; ISON, Craig H.;  
 ; APPLICANT: RAMKUMAR, Jayalaxmi; TANQ, Y. Tom;  
 ; APPLICANT: LAL, Preeti G.; BOROMSKY, Mark L.;  
 ; APPLICANT: DUGGAN, Brendan M.; HAFALIA, April J.A.;  
 ; APPLICANT: ARVIZU, Chandra S.; THANGAVELU, Kavitha;  
 ; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;  
 ; APPLICANT: DING, Li; YUE, Henry;  
 ; APPLICANT: LEE, Sally; SWARNAKAR, Anita;  
 ; APPLICANT: TRAN, Uyen K.; XU, Yuming  
 ; TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES  
 ; FILE REFERENCE: PI-0361 USN  
 ; CURRENT APPLICATION NUMBER: US/10/467,042  
 ; CURRENT FILING DATE: 2003-07-31  
 ; PRIOR APPLICATION NUMBER: PCT/US02/02813  
 ; PRIOR FILING DATE: 2002-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/265,705  
 ; PRIOR FILING DATE: 2001-01-31  
 ; PRIOR APPLICATION NUMBER: US 60/266,762  
 ; PRIOR FILING DATE: 2001-02-05  
 ; PRIOR APPLICATION NUMBER: US 60/269,581  
 ; PRIOR FILING DATE: 2001-02-16  
 ; PRIOR APPLICATION NUMBER: US 60/271,198  
 ; PRIOR FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: US 60/272,813  
 ; PRIOR FILING DATE: 2001-03-01  
 ; PRIOR APPLICATION NUMBER: US 60/275,586  
 ; PRIOR FILING DATE: 2001-03-13  
 ; PRIOR APPLICATION NUMBER: US 60/278,505  
 ; PRIOR FILING DATE: 2001-03-23  
 ; PRIOR APPLICATION NUMBER: US 60/280,539  
 ; PRIOR FILING DATE: 2001-03-30  
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 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 27  
 ; LENGTH: 4506  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incycle ID No: 7473634CB1  
 US-10-467-042-27  
 Query Match 14.2%; Score 1442.8; DB 16; Length 4506;  
 Best Local Similarity 66.0%; Pred. No. 0;  
 Matches 2182; Conservative 0; Mismatches 1042; Indels 84; Gaps 3;

QY 103 CTAGTCAAGAGCAATTTGAGTTGAAGTCTCGAGGTGTGAAGTGTATGCCAGCAAGAC 162  
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 QY 163 AACAGCCAGAGAAGCGTGTGTTAACTCAGGTTGTGTGTCCCAAGACATATATGTGT 222  
 DB 583 GGAAGCCATTAATACTGTGTCTTGAAGCCAAAGAGGTTCATGTGTCTGACATGTGT 642  
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QY 283 AGCTTCAGATTGACCTGCAACGAGGCTATGACCTGCAAGGGCTCCAGGGATCACTCGT 342  
DB 703 AATGTAAGATTTTCAATGAGAGCAATTAAGTCTCCAGGATCTTAAAGCATCACTCGT 762  
QY 343 ATGAAAGTGAAGCAATGTTTGCAGCTGAGAGCAACAGAGCCAGTCTGCGAGCCCGC 402  
DB 763 CAGAGAGTTACAGAGACGCTGCTGTTGAGTGAACACAGGCCATCTGCGAGACGAGA 822  
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DB 1999 AGATTCAAAACCGAGTCAACTATGACACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2058  
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DB 2179 CACTATGAGTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2238  
QY 1903 GGAAGGCTCATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1962  
DB 2239 GGCATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2298  
QY 1963 GGCATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2022  
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QY 2023 GGCATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2082  
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 Db 3139 ATCTTAAACAGCACATCCATCACTGTGTGCTGAGTTCAACCAATGATCTGACACC 3198  
 QY 2863 AGCAAGGCTTTAATCTGCACTTTTCCAGTTTGAATCAATATGATGAGACCCAGGA 2922  
 Db 3199 GACCAAGGTTTAACTCACTATACAGTTTGAATCTGTTAAATGTGAGATCCGGGG 3258  
 QY 2923 ACCCCCAAGTTGGCTACAAAGTTTCAATGATGAAGTCAATTTTCAGGAGACCTCGTGC 2982  
 Db 3259 ATCCCTAACATGAGGCTATGAGATCCGTATGAAAGCCACTTTTCCAGACATGATGTTCTG 3318  
 QY 2983 TTCACTGTGACCTCTGATACAGCTTGGGGGTAGTGAAGAGCTGTGTCTGATGGA 3042  
 Db 3319 TACAGTTGCAACCCGGGGTACGCCATGATGAGCAACCCCTGACCTGTTTGAATGGA 3378  
 QY 3043 GAGCGCGGACCTGGGACCGGCTCTGCCCACCTGTGTGCGCCAGTGTGAGAGGAGCA 3102  
 Db 3379 GACAGAGAGTGTGGGACAAACCACTACCTTCTGTGATACCGGAATGTGTGTGATGATC 3438  
 QY 3103 AGAGAGAGGCTGTGGGGGACGTGTCTGACCCGGGATCCAGCTCCCTATGAACAAAT 3162  
 Db 3439 CATGACGCCAATCAGAGCAATATTTGCTCCCTGGCTATCTCACTCCGATGCAACAC 3498  
 QY 3163 CTCACATGCACTTGAACCATGAGGAGAGGCGGCTGACCATTTGGGCTACACTTCTG 3222  
 Db 3499 CTCACATGCACTTGAATTAAGAGGAGAGCCAGGAAGCATTTAGCTTCATTTCAAT 3558  
 QY 3223 GTGTGTGACAGAGAGGTTTCAAGAGTGTGCGCATCTGGGATGGGCTGTGAGAGC 3282  
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 Db 3619 GACATCTGTGTGAAGAGTGAATGTGCTCGCCCTTCGAGGACATCCACACACTTC 3678  
 QY 3343 AACTCGGTGCTCTGAGAGTTCAGCACTGAATTTCTTCAACGAGAGGAGGCTTGGCAAT 3402  
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RESULT 13  
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 ; Sequence 69, Application US/10398037  
 ; Publication No. US20040138414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS; YUE, Henry;

; APPLICANT: TANG, Y. TOM; NGUYEN, DANNIEL B.;  
 ; APPLICANT: YAO, Monique G.; XU, Yuming;  
 ; APPLICANT: TRIBOULEY, Catherine M.; SAMJAWALA, Madhusudan M.;  
 ; APPLICANT: CHAMLA, Narinder K.; BAUGHN, Mariah R.;  
 ; APPLICANT: SAPIERSTEIN, Stephanie K.; LAL, Preeti G.;  
 ; APPLICANT: THORNTON, Michael B.; GANDHI, Ameeta R.;  
 ; APPLICANT: RAMKUMAR, Jayalaxmi; ELIOT, Vicki S.;  
 ; APPLICANT: ARVIZU, Chandra S.; THANGAVELU, Kavitha;  
 ; APPLICANT: GIETZEN, Kimberly J.; DING, Li;  
 ; APPLICANT: AU-YOUNG, Janice K.; TRAN, Bao;  
 ; APPLICANT: POLICKY, Jennifer L.; LEE, Sally;  
 ; APPLICANT: LU, Dying Aina M.; BURFORD, Neil;  
 ; APPLICANT: WARREN, Bridget A.; GURURAJAN, Rajagopal;  
 ; APPLICANT: DUGGAN, Brendan M.; HONCHELL, Cynthia D.;  
 ; APPLICANT: HARALIA, April J.A.  
 ; TITLE OF INVENTION: SECRETED PROTEINS  
 ; FILE REFERENCE: PI-0240 USN  
 ; CURRENT APPLICATION NUMBER: US/10/398,037  
 ; CURRENT FILING DATE: 2003-03-28  
 ; PRIOR APPLICATION NUMBER: PCT/US01/30042  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: US 60/242,218  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: US 60/236,869  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: US 60/239,812  
 ; PRIOR FILING DATE: 2000-10-11  
 ; PRIOR APPLICATION NUMBER: US 60/240,108  
 ; PRIOR FILING DATE: 2000-10-12  
 ; PRIOR APPLICATION NUMBER: US 60/241,282  
 ; PRIOR FILING DATE: 2000-10-17  
 ; NUMBER OF SEQ ID NOS: 136  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 69  
 ; LENGTH: 2387  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; OTHER INFORMATION: Incyte ID No: 6813464CB1  
 ; US-10-398-037-69  
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 Best Local Similarity 90.5%; Pred. No. 0;  
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 Db 61 GCTAGCAATCAGGACACTTCCGTGGGCGTGAAGACCTCCGAGCTAGTCAAGAAACAATT 120  
 QY 121 GAGTTGAATCTCGAGGTGTGAAGCTGATGCCAGCAAGAAACAAGCAAGAGCTCT 180  
 Db 121 GAGTTGAATCTCGAGGTGTGAAGCTGATGCCAGCAAGAAACAAGCAAGAGCTCT 180  
 QY 181 GTGTTAATCAGAGTTGTGTGTCCCAAGGACATAATATATGTGTCCAGACCTGGCATACC 240  
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 QY 301 AAAGAGGCTATGACCTGCAAGGCTCCAGCGGATACCTGTATGAAGTGAAGCGGACATG 360  
 Db 301 AAAGAGGCTATGACCTGCAAGGCTCCAGCGGATACCTGTATGAAGTGAAGCGGACATG 360  
 QY 361 TTGGCGGCTGAGAGCAGACAGGCGGCTGTCCGAGCCCGGATGTGTATGCCACCTT 420  
 Db 361 TTGGCGGCTGAGAGCAGACAGGCGGCTGTCCGAGCCCGGATGTGTATGCCACCTT 420



Db	300	GAAAGCTGGCAGGGCTACTTGGTGAATGAATGTGTGCTTTCCAGTGTAGCCGGGATA	359
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Db	360	TGCCCTCCAGGGCCACGCCCAATCTCTGCATGCCCGGAAACAGTGGCGGATGAACTA	419
QY	5154	CCCTTCCTCACTCTGTATTTGCAACAATGTGGGGGAAACAATGGAGGAGATGAGGGGGTGTAT	5213
Db	420	CCCTTCCTCACTCTGTATTTGCAACAATGTGGGGGAAACAATGGAGGAGATGAGGGGGTGTAT	479
QY	5214	CCTGAGCCCCGGGCTTCCAGGGCAACTACCCAGTAACTGGAATGCTCTCTGAAAATATAGC	5273
Db	480	CTTGAGCCCCGGGCTTCCAGGGCAACTACCCAGTAACTGGAATGCTCTCTGAAAATATAGC	539
QY	5274	ACTGCCCCGTGGGCTTTGGAGCTCAATCAAGTTCCTGAACTTCTTCAACCGAGCCAAACA	5333
Db	540	ACTGCCCCGTGGGCTTTGGAGCTCAATCAAGTTCCTGAACTTCTTCAACCGAGCCAAACA	599
QY	5334	CGACTCACTAGAAATCCGGAAATGGCCCTTATGAGACACGCGCATGATGGAGATTGAG	5393
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Db	900	CACGTGTCAACATGGACCAACACCGGAACTGGGACACACCCCTGCCCAAGTGTGAAGTCC	959
QY	5694	TTGTGGCGGGAACATCACTTCTTCCAAACGGAACGTGTGTACTTCCCGGGGTTTCCCTAGCC	5753
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QY	5754	GTACTCCAGCTTCCAGGACTGTGTCTGGCTGATCAACGTGCCATTGGCCATGGCGTCCG	5813
Db	1020	GTACTCCAGCTTCCAGGACTGTGTCTGGCTGATCAACGTGCCATTGGCCATGGCGTCCG	1079
QY	5814	CCTCAACCTCAGCCCTGTGCAGACAGAGCCCTGTGGAATTTCAATCAACATCTGGGATGG	5873
Db	1080	CCTCAACCTCAGCCCTGTGCAGACAGAGCCCTGTGGAATTTCAATCAACATCTGGGATGG	1139
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Db	1260	CTTGCCCATAGCTTCTCCGCTTCA 1283	

```

APPLICANT: INCYTE CORPORATION
APPLICANT: BAUGHN, Mariah R.
APPLICANT: DING, Li
APPLICANT: ELIOTT, Vicki S.
APPLICANT: GANDHI, Ameena R.
APPLICANT: GIETZEN, Kimberly J.
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: HARALLA, April J.A.
APPLICANT: KEARNEY, Liam
APPLICANT: KHAN, Farrah A.
APPLICANT: LAL, Preeti G.
APPLICANT: LEE, Ernestine A.
APPLICANT: LU, Dyrng Aina M.
APPLICANT: LU, Yan
APPLICANT: NGUYEN, Daniel B.
APPLICANT: ARVIZU, Chandra S.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: TANG, Y. Tom
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THORNTON, Michael B.
APPLICANT: CHAMLA, Narinder K.
APPLICANT: WARREN, Bridget A.
APPLICANT: XU, Yuming
APPLICANT: YAO, Monique G.
APPLICANT: YUE, Henry

TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0827 USN
CURRENT FILING DATE: US/10/399,455
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: PCT/US01/32090
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,871
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/244,723
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 60/249,402
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/252,622
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/255,622
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PERL Program
SEQ ID NO 31
LENGTH: 2609
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7473630CBI
US-10-399-455-31

Query Match 7.7%, Score 783.6; DB 17; Length 2609;
Best Local Similarity 62.1%; Pred. No. 6,2e-22;
Matches 125; Conservative 0; Mismatches 764; Indels 3; Gaps 1;

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Db 637 CTTTTCATATGACAAATACCTGCGTTCGATGTGATGATGAGGTAGATCTTGGAAATA 696
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Db 697 TTGCAGCTTCAGATTTCTTCTTTTGTGTAACGGAAGATCACAATATATCTCCGAGTCT 756
QY 3263 GGGATGGGCTCTGTGAGAGCGGGGTTCTGCTGAAGAGAGCTGAGTGGCCCGGCGCTGCCCA 3322
Db 757 GGGAGCGGTCCACGAAATATATATGCTTTTAAAGAAATTAAGTATGATCTCTTAATTCCTG 816

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 DB 1717 TAGCAGTTCCAAGAGGAGT 1773  
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 DB 1834 CAGGATCCCATACAGAGGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1893  
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DB 1894 TTAATGTGCAAGGATATGT 1953  
 QY 4463 GAAACAGGCGCAAGGATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4522  
 DB 1954 GAAACAGGCGCAAGGATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2013  
 QY 4523 GTGACTTCTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4582  
 DB 2014 ATGAAATTTGCAAGTGTGATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2073  
 QY 4583 GGTGCGAGAGATGAGTGTGCT 4642  
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 QY 4643 CGCCCAAGT 4702  
 DB 2134 TACCTACTTGT 2193  
 QY 4703 CCCCTGCTTCCAGAGGCGTACCTCAACAGCTCAACTGTGTGTGTGTGTGTGTGTGTGTGT 4762  
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